Best Available Copy U.S. DEPARTMENT OF COMMERCE SEARCH REQUEST FORM Requestor's Serial Name: Number: 08/9/8874 5-14-98 108-4008 Art Unit: _/6 46 Search Topic: Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s). Plane sand SEQJDLO: 1 + 2 of 08/918874. STAFF USE ONLY Search Site Vendors IG Suite Terminal time: CM-1 Elapsed time: __ Pre-S Dialog CPU time: Type of Search APS Total time: N.A. Sequence Geninfo Number of Searches: A.A. Sequence SDC Number of Databases: Structure DARC/Ouestel Other M/32 Bibliographic

PTO-1590 (9-90) * U.S. GPO: 1995-398-798/22469

USCOMM-DC 90-3952



Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri May 15 17:45:22 1998; MasPar time 2128.68 Seconds 1495.787 Million cell updates/sec

Tabular output not generated.

Title. >US-08-918-874-2

Description: (1-2082) from US08918874.seq

Perfect Score: 2082

N.A. Sequence: 1 CCAACTGCACCTCGGTTCTA.....CATTTTATATTGCTTTACTA 2082 Comp: GGTTGACGTGGAGCCAAGAT......GTAAAATATAACGAAATGAT

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb153

1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg

7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi 13:em_pat

Database: genbank105

14:gb_ro 15:qb_om 16:qb_ov 17:qb_in 18:qb_pl 19:qb_ba 20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat

26:qb_htq 27:qb_pr1 28:qb_pr2

Statistics: Mean 11.767; Variance 5.428; scale 2.168

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1776	85.3	1804	28	AF029761	Homo sapiens decov rec	0.00e+00
2	1161	55.8	1161	28	AF023849	Homo sapiens TNF recep	0.00e+00
3	390	18.7	1180	28	AF012536	Homo sapiens decoy rec	0.00e+00
4	390	18.7	1377	28	AF033854	Homo sapiens lymphocyt	0.00e+00
5	388	18.6	900	28	AF020502	Homo sapiens cytotoxic	0.00e+00
6	386	18.5	1388		AF016267	Homo sapiens TRAIL rec	0.00e+00
7	345	16.6	780	28	AF012629	Homo sapiens antagonis	1.22e-273
8	264	12.7	1323	28	AF018658	Homo sapiens apoptosis	3.16e-200
9	265	12.7	3993	28	AF016266	Homo sapiens TRAIL rec	3.97e-201
10	259	12.4	1859	28	AF016849	Homo sapiens apoptosis	1.01e-195
11	202	9.7	1407		HSU90875	Human cytotoxic ligand	
12	195	9.4	1236		AF020501	Homo sapiens cytotoxic	
13	195	9.4	1236		AF018657	Homo sapiens apoptosis	1.75e-138
14	196	9.4	1717	28	AF016268	Homo sapiens death rec	2.27e-139

	15	194	9.3 1799 2	8 AF012535	Homo sapiens death rec	1.35e-137
	16	191	9.2 1236 2		Homo sapiens death dom	6.14e-135
	17	191	9.2 1236 2		Homo sapiens p53-regul	6.14e-135
	18	96		8 AC002369	Homo sapiens Xp22 PAC	8.54e-53
	19	93		8 HS102G20	Human DNA sequence fro	2.63e-50
	20	93		6 AC004031	Homo sapiens; HTGS pha	2.63e-50
	21	93	4.5 149490 2	28 HSU95740	Human chromosome 16p13	2.63e-50
	22	94		28 AC002449	Human PAC clone DJ404K	3.90e-51
С	23	92	4.4 63369 2	26 AC002413	*** SECUENCING IN PROG	1.77e-49
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С	25	91	4.4 153460 2	28 HSU52111	Homo sapiens Xq28 geno	1.18e-48
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С	29	89	4.3 40491 2	28 AC002116	Human DNA from chromos	5.25e-47
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1804)

AUTHORS Marsters, S.A., Sheridan, J.P., Pitti, R.M., Huang, A., Skubatch, M., Baldwin, D., Yuan, J., Gurney, A., Goddard, A.D., Godowski, P. and Ashkenazi.A. A Novel Receptor for Apo2L/TRAIL Contains a Truncated Death Domain TITLE

JOURNAL Curr. Biol. (1997) In press

REFERENCE 2 (bases 1 to 1804) Marsters, S.A., Sheridan, J.P., Pitti, R.M., Huang, A., Skubatch, M., AUTHORS Baldwin, D., Yuan, J., Gurney, A., Goddard, A.D., Godowski, P. and

Ashkenazi, A. TITLE Direct Submission

JOURNAL Submitted (14-OCT-1997) Molecular Oncology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA

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REFERENCE
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 AUTHORS
         Pan.G.
 TITLE
          TRUNDD, a new member of the TRAIL receptor family that antagonizes
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 JOURNAL
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REFERENCE
         2 (bases 1 to 1161)
 AUTHORS
          Pan, G., Ni, J. and Dixit, V.M.
 TITLE
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 JOHRNAL.
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                 Sheridan, J.P., Marsters, S.A., Pitti, R.M., Gurney, A., Skubatch, M.,
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                 Goddard, A.D., Godowski, P. and Ashkenazi, A.
  TITLE
                 Control of TRAIL-induced apoptosis by a family of signaling and
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  JOURNAL.
                Science 277 (5327), 818-821 (1997)
  MEDLINE
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REFERENCE
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  AUTHORS
                Sheridan, J.P., Marsters, S.A., Pitti, R.M., Gurney, A., Baldwin, D.,
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  TITLE
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 AUTHORS
           Mongkolsapaya, J., Cowper, A., Xu, X., Morris, G., McMichael, A.J.,
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           Lymphocyte inhibitor of TRAIL: A new receptor protecting
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           lymphocytes from the death ligand TRAIL
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REFERENCE
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DEFINITION Homo sapiens lymphocyte inhibitor of TRAIL (LIT) mRNA, complete

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 AUTHORS
         Pan,G., Ni,J., Wei,Y.F., Yu,G., Gentz,R. and Dixit,V.M.
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          An antagonist decoy receptor and a death domain-containing receptor
 JOURNAL
          Science 277 (5327), 815-818 (1997)
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          Pan, G., Ni, J., Wei, Y., Yu, G., Gentz, R. and Dixit, V.M.
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          Characterization of two receptors binding TRAIL
          FEBS Lett. (1997) In press
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          Walczak, H., Degli-Esposti, M.A., Johnson, R.S., Smolak, P.J.,
          Waugh, J.Y., Boiani, M., Timour, M.S., Gerhart, M.J., Schooley, K.A.,
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          The receptor for the cytotoxic ligand TRAIL
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          Science 276 (5309), 111-113 (1997)
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Db

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Db

Qy

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Dh

Qy

Dh

Qy

Db

Qy

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RESULT 14

ACCESSION

AUTHORS

JOURNAL Immunity 7 (6), 821-830 (1997)

TITLE

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          Chaudhary, P.M., Eby, M., Jasmin, A., Bookwalter, A. and Hood, L.
          Direct Submission
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                   Control of TRAIL-induced apoptosis by a family of signaling and
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Job time : 2268 secs.

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Release 3.0.5AA John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1997 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:48:14 1998: MasPar time 19.72 Seconds 824.206 Million cell updates/sec

Tabular output not generated.

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Description: (1-386) from US08918874.pep

Perfect Score: 2715

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Scoring table: PAM 150

Gap 11

Searched: 140555 segs, 42109429 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: sptremb15

Pagn1+

1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mamma1 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate

13:sp_unclassified

Statistics: Mean 47.012; Variance 94.359; scale 0.498

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 2	1060 1044	39.0 38.5	440 440	2 2	015531 014763	APOPTOSIS INDUCING PRO APOPTOSIS INDUCING REC	1.72e-185 3.54e-182
3	834	30.7	299	2	014798	CYTOTOXIC TRAIL RECEPT	
4	820	30.2	259	2	014755	TRAIL RECEPTOR 3.	4.69e-136
5	811	29.9	411	2	015517	CYTOTOXIC TRAIL RECEPT	3.25e-134
6	804	29.6	411	2	014720	DEATH RECEPTOR 5.	8.74e-133
7	795	29.3	411	2	015508	P53-REGULATED DNA DAMA	6.02e-131
8	784	28.9	468	2	000220	CYTOTOXIC LIGAND TRAIL	1.06e-128
9	192	7.1	471	4	019131	TUMOR NECROSIS FACTOR-	3.21e-14
10	191	7.0	459	10	Q62327	TUMOR NECROSIS FACTOR	4.71e-14
11	187	6.9	348		Q85407	HOMOLOG OF VACCINIA VI	
12	187	6.9	349		Q89098	GARCIA-1966 RIGHT NEAR	2.16e-13
13	187	6.9	349		Q89118	SOMALIA-1977 RIGHT NEA	2.16e-13
14	186	6.9	355		Q85308	SECRETED RECEPTOR BIND	
15	182	6.7	314	2	Q14293	FAS SOLUBLE PROTEIN.	1.44e-12
16	176	6.5		10	Q63199	FAS ANTIGEN PRECURSOR.	
17	176	6.5		10	008727	OSTEOPROTEGERIN.	1.36e-11
18	175	6.4		10	008712	OSTEOPROTEGERIN:	1.97e-11
19	167	6.2	401	2	000300	OSTEOPROTEGERIN.	3.78e-10
20	157	5.8	283	2	Q92956	HERPESVIRUS ENTRY MEDI	1.41e-08

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36	109	4.0		065274	J13L GENE (ISOLATE TAN	1.15e-01
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RA	SCREATON G.R., MONGKOLSAPAYA J., XU X., COWPER A.E., MCMICHAEL A.J.,
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RA	SCHNEIDER P., BODMER JL., THOME M., HOLLER N., HOPMANN K.,
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RL	FEBS LETT. 0:0-0(1997).
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121 CKSGOTNKSSCTTTRDTVCOCEKGSFODKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKC 180 Qy

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                                                                                       MACFARLANE M., AHMAD M., SRINIVASULA S.M., FERNANDES-ALNEMRI T.,
     RA
                                                                                       COHEN G.M., ALNEMRI E.S.:
                                                                                   RI.
                                                                                       J. BIOL. CHEM. 0:0-0(1997).
                                                                                       EMBL: AF020502: G2443820: -.
                                                                                   SO SEQUENCE 299 AA: 31759 MW: 59B93A14 CRC32:
RESILT.
ID 014763
                 PRELIMINARY; PRT; 440 AA.
                                                                                                        30.7%; Score 834; DB 2; Length 299;
                                                                                     Best Local Similarity 61.9%; Pred. No. 6.40e-139;
                                                                                     Matches 130; Conservative 27; Mismatches 50; Indels 3; Gaps 3;
    014763:
    01-JAN-1998 (TREMBLREL, 05, CREATED)
    01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)
                                                                                          11 LGNSGDRAPRPPDGR-GRVRPRTQDGVGNHTMARIPKTLKFVVVIVAVLLPVLAYSATTA 69
                                                                                          01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
    APOPTOSIS INDUCING RECEPTOR TRAIL-R2.
                                                                                   Qy
    TRATLE2.
    HOMO SAPIENS (HUMAN).
                                                                                         70 ROBEVPOOTVAPOOORHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCT 129
                                                                                   nh
    EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
                                                                                            nismiimmiilisis muunka mukuunu sur mis u
    EUTHERIA: PRIMATES.
                                                                                          60 RODEVPOOTVAROOORRSIKERECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLICT 119
00
                                                                                   Qy
RN
    [1]
    SEQUENCE FROM N.A.
                                                                                        130 VCKSDOKHKSSCTMTRDTVCOCKEGTFRNENSPEMCRKCSR-CPSGEVOVSNCTSWDDIO 188
ΡD
                                                                                   Νħ
    WALCZAK H., DEGLI-ESPOSTI M.A., JOHNSON R.S., SMOLAK P.J., WAUGH J.Y.,
                                                                                            100 Î :000 1000Î 1:1:: 0000 E -11 E 1000: 0
    BOIANI M., TIMOUR M.S., GERHART M.J., SCHOOLEY K.A., SMITH C.A.,
                                                                                   0v
                                                                                        120 VCKSGOTNKSSCTTTRDTVCOCEKGSRODKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIK 179
    GOODWIN R.G., RAUCH C.T.;
    EMBO J. 16:5386-5397(1997).
                                                                                        189 CVEEFGANATVETPAAEETMNTSPGTPAPA 218
                                                                                   ηh
                                                                                            Talalat HIIII L. La
    SEQUENCE FROM N.A.
                                                                                        180 CKNESAASSTGKTPAARETVTTILGMLASP 209
RP
RA
    WALCZAK H.:
    SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
    EMBL: AF016849: G2465586: -.
                                                                                   RESULT 4
   SEQUENCE 440 AA; 47850 NW; 268DA232 CRC32;
                                                                                   TD 014755
                                                                                                    PRELIMINARY: PRT: 259 AA.
  Query Match 38.5%; Score 1044; DB 2; Length 440; Best Local Similarity 52.7%; Pred. No. 3.54e-182;
                                                                                       01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
                                                                                   DΤ
  Matches 184; Conservative 54; Mismatches 91; Indels 20; Gaps 9;
                                                                                   DΤ
                                                                                       01-JAN-1998 (TREMBLREL, 05, LAST ANNOTATION UPDATE)
       1 MEORGONAPAASGARKRHGPGPREARGARP---GPRVPKTLVLVVAAVLLLVSAESALIT 57
                                                                                       TRAIL RECEPTOR 3.
       | :||: |:||:|| :||:|| |:|| |::| |::|| ||| | :|| | 1 MGLWGOSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVA-VLLPVRVDSATIP 59
                                                                                   0S
                                                                                       HOMO SAPIENS (HUMAN).
                                                                                   OC.
                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                   OC
                                                                                       EUTHERIA: PRIMATES.
Νh
      58 QQDLAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCLRCT 117
                                                                                   RN
      RP
                                                                                       SEQUENCE FROM N.A.
                                                                                   RC
                                                                                       TISSUE=LIVER AND SPLEEN:
                                                                                       SCHNEIDER P., BODMER J.-L., THOME M., HOLLER N., HOFMANN K.,
                                                                                       TSCHOPP J.;
     118 RCDSGEVELSPCTTTRNTVCOCKEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIK 177
                                                                                   RA
                                                                                       FEBS LETT. 0:0-0(1997)
          RT.
     120 VCKSGOTNKSSCTTTRDTVCOCRKGSFODKNSPRMCRTCRTGCPRGMVKVSNCTPRSDIK 179
                                                                                   DR EMBL: AF016267: G2529565: -.
                                                                                   SO SEQUENCE 259 AA; 27365 MW; 3C196935 CRC32;
     178 CVHKESGTKHSGEAPAVEETVTSSPGTPASPCSLSGIIIGVTVAAVVLIVAVFVCKSLLW 237
Dh
                                                                                                         30.2%; Score 820; DB 2; Length 259;
         180 C-KNESAASSTGKTPAAEETVTTILGMLASPYHYL-IIIVVLVIILAVVVVGFSCR---- 233
                                                                                     Best Local Similarity 69.7%; Pred. No. 4.69e-136;
Qу
                                                                                     Matches 122: Conservative 18: Mismatches 34: Indels 1: Gaps 1;
     238 KKVLPYLKGICSGGGDPERVDR-----SSO-R-PGAEDNVLNEIVSI--LOPTOVPEO 287
         5 PKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTG 64
     234 KKFISYLKGICSGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLOPTOVSEO 293
                                                                                            11 (1001-1000) - 10 (11:000) (10:00) (10:00) (10:00)
                                                                                          35 PKILKEVVETVAVLLPVRVDSATIPRODEVPOOTVAPOOORRSLKEEECPAGSHRSEYTG 94
     288 EMEVOEPAEPTGVNMLSPGESEHLLEPAEAERSORRRLLVPANEGDPTE 336
         te ii ii iii ii : T teelii iiii iiiiiiii tetee
                                                                                         65 ACNPCTRGVDYTNASNNEPSCPPCTVCKSDOKHKSSCTMTRDTVCOCKEGTFRNVNSPEM 124
                                                                                   Πh
     294 EIOGORLAEL/TGVTVEXPEEPORLLEOAEAEGCORRELL/VPVNDADSAD 342
                                                                                            Qy
                                                                                         95 ACNPCTRGVDYTIASNNLPSCLLCTVCKSGOTNKSSCTTTRDTVCOCEKGSFODKNSPEM 154
RESULT 3
                                                                                        125 CRKCSR*CPSGEVOVSNCTSWDDIOCVEEFGANATVETPAAEETMNTSPGTPAPA 178
ID 014798
                 PRELIMINARY; PRT; 299 AA.
                                                                                            155 CRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASP 209
    01-JAN-1998 (TREMBLREL. 05, CREATED)
    01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)
                                                                                   RESULT 5
    01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                   TD 015517
                                                                                                    PRELIMINARY: PRT: 411 AA.
DE CYTOTOXIC TRAIL RECEPTOR-3.
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AC 015517:
    01-JAN-1998 (TREMBLREL, 05, CREATED)
    01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
    01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
    CYTOTOXIC TRAIL RECEPTOR-2.
    DR5 OR TRICK2A.
    HOMO SAPIENS (HUMAN).
    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
ന
    EUTHERIA; PRIMATES.
RN
    SEQUENCE FROM N.A.
RP
    MACFARLANE M., AHMAD M., SRINIVASULA S.M., FERNANDES-ALNEMRI T.,
                                                                                    Qy
    COHEN G.M., ALNEMRI E.S.;
RT.
    J. BIOL. CHRM. 0:0-0(1997).
RN
RD
    SEQUENCE FROM N.A.
    SCREATON G.R., MONGKOLSAPAYA J., XU X., COMPER A.E., MCMICHAEL A.J.,
RA
    BELL A.J.:
    CURR. BIOL. 0:0-0(1997).
    EMBL; AF020501; G2443818; -.
    EMBL; AF018657; G2407651; -.
    SEQUENCE 411 AA: 45127 MW: 579FB4AD CRC32:
                    29.9%; Score 811; DB 2; Length 411;
  Best Local Similarity 50.6%; Pred. No. 3.25e-134;
  Matches 173; Conservative 52; Mismatches 82; Indels 35; Gaps 12;
       1 MEQRGQNAPAASGARKRHGPGPREARGARPGLRVPKTLVLVV--AAVLLLVSAESALITO 58
        1 MGLWGOSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPR 60
                                                                                    RESULT 7
Db
      59 ODLAPOORVAPOOKRSSPSEGLCPPGHHISEDGRDCISCKYGODYSTHWNDLLFCLRCTR 118
                                                                                    ID 015508
      Qy
Dh
     119 CDSGEVELSPCTTTRNTVCOCEEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIEC 178
         1 H: : 1:000:000 1:0:: :0000 10000000:00:00 1
     121 CKSGOTNKSSCTTTRDTVCOCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKC 180
Qy
                                                                                    DE
                                                                                    GN KILLER OR DRS.
     179 VH------K----ESGI--IIGV--T-----VAAVVLIVAV-FVCKSLL-WKKVLPYL 215
             00
     181 KNESAASSTGKTPAARETYTTILGMLASPYHYLIIIVVLVIILAVVVVGFSCRKKFISYL 240
Qy
                                                                                    OC.
                                                                                        [1]
                                                                                    RN
     216 KGICSGGGDPERVDR-----SSQ-R-PGAEDNVLNEIVSI--LQPTQVPEQEMEVQEP 265
                                                                                    RP
         monucus e a concer e continua
                                                                                    RC
                                                                                        TISSUE=OVARIAN:
     241 KGICSGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLOPTOVSROEIOGOFL 300
                                                                                    RA
Dh
     266 AEPTGVNMLSPGESEHLLEPAEAERSORRRLLVPANEGDPTE 307
                                                                                    RN
         HORE TERRITOR HINDER FREE
                                                                                    RP
     301 AELTGVTVEXPEEPQRLLEQAEAEGCQRRRLLVPVNDADSAD 342
                                                                                    RX
PRCIILT 6
ID 014720
                 PRELIMINARY; PRT; 411 AA.
    01-JAN-1998 (TREMBLREL, 05, CREATED)
    01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
    01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
    DEATH RECEPTOR 5.
DR
GN
    DRS
0S
    HOMO SAPIENS (HUMAN).
OC
    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC
    EUTHERIA: PRIMATES.
RN
    [1]
RP
    SEQUENCE FROM N.A.
    MEDLINE: 97390509.
                                                                                    Ω۷
    SHERIDAN J.P., MARSTERS S.A., PITTI R.M., GURNEY A., SKUBATCH M.,
    BALDWIN D., RAMAKRISHNAN L., GRAY C.L., BAKER K., WOOD W.I.,
    GODDARD A.D., GODOWSKI P., ASHKENAZI A.:
    SCIENCE 277:818-821(1997).
                                                                                    Q٧
    EMBL: AF012535: G2338420: -.
    SEQUENCE 411 AA; 45081 MW; 89F2F042 CRC32;
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Query Match 29.6%; Score 804; DB 2; Length 411; Best Local Similarity 50.3%; Pred. No. 8.74e-133;
 Matches 172; Conservative 52; Mismatches 83; Indels 35; Gaps 12;
      1 MEQRGQNAPAASGARKRHGPGPREARGARPGLRVPKTLVLVV--AAVLLLVSAESALITO 58
      59 ODLAPOORAAPOOKRSSPSEGLCPPGHHISEDGRDCISCKYGODYSTHWNDLLFCLRCTR 118
        61 ODEVPOOTVAPOOORRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTV 120
    119 CDSGEVELSPCTTTRNTVCOCERGTFREEDSPENCRKCRTGCPRGMVKVGDCTPWSDIEC 178
        1.11: : 1:1091:1000 1:1:: :3000 00000000::01:01 1
    121 CKSGOTNKSSCTTTRDTVCOCEKGSPODKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKC 180
    179 VH------K----ESGI--IIGV--T-----VAAVVLIVAV-FVCKSLL-WKKVLPYL 215
              - I - I : I:I: : : : III:: : I :: :II ::II
    181 KNESAASSTGKTPAARETVTTILGMLASPYRYLIIIVVLVIILAVVVVGPSCRKKFISYL 240
    216 KGICSGGGGDPERVDR-----SSO-R-PGAEDNVLNEIVSI--LOPTOVPEOEMEVOEP 265
        241 KGICSGGGGPERVHRVLFRRRSCPSRVPGARDNARNETLSNRYLOPTOVSEORIOGORL 300
    266 AEPTGVNMLSPGESEHLLEPAEAERSORRRLLVPANEGDPTE 307
        HIARD COLUMN TO A STREET
    301 AELTGVTVEXPEEPORLLEOAEAEGCORRRLLVPVNDADSAD 342
              PRELIMINARY; PRT; 411 AA.
   01-JAN-1998 (TREMBLREL. 05, CREATED)
   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
    01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
   P53-REGULATED DNA DAMAGE-INDUCIBLE CELL DEATH RECEPTOR.
   HOMO SAPIENS (HUMAN).
   EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
   EUTHERIA: PRIMATES.
   SEQUENCE FROM N.A.
   WU G.S., EL-DEIRY W.S.:
   NAT. GENET. 16:0-0(1997).
   SEQUENCE FROM N.A.
   MEDLINE; 97390508.
RA PAN G., NI J., WEI Y.F., YU G., GENT2 R., DIXIT V.M.;
   SCIENCE 277:815-818(1997).
   EMBL: AF022386: G2460428: -.
   EMBL; AF012628; G2338429; -.
SQ SEQUENCE 411 AA; 45083 MW; 09B03B74 CRC32;
 Query Match 29.3%; Score 795; DB 2; Length 411; Best Local Similarity 49.6%; Pred. No. 6.02e-131;
 Matches 170; Conservative 56; Mismatches 80; Indels 37; Gaps 13;
      1 MEQRGQNAPAASGARKRHGPGPREARGARP --- GPRVPKTLVLVVAAVLLLVSAESALIT 57
      58 OODLAPOORAAPOOKRSSPSEGLCPPGHHISEDGRDCISCKYGODYSTHWNDLLFCLRCT 117
     118 RCDSGEVELSPCTTTRNTVCOCEEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIE 177
         120 VCKSGQTNKSSCTTTRDTVCQCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIK 179
    178 CVH------K----ESGI--IIGV--T-----VAAVVLIVAV-FVCKSLL-WKKVLPY 214
```

EUTHERIA: ARTIODACTYLA.

6 11 2

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180 CKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIILAVVVVGFSCRKKFISY 239
                                                                                    RP SEQUENCE FROM N.A.
                                                                                    RC TISSUE=AORTA:
     215 LKGICSGGGDPERVDR-----SSQ-R-PGAEDNVLNEIVSI--LQPTQVPEQEMEVQE 264
                                                                                     RA LEE E.-K., TALYOR M.J., KEHRLI M.E.;
                                                                                    RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
         manin ma ca a famo na dinimina in
     240 LKGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLOPTOVSEOEIOGOE 299
                                                                                    DR EMBL: U90937; G2290398; -.
                                                                                    DR PROSITE; PS00652; TNFR_NGFR_1; 3.
                                                                                    SO SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;
     265 PAEPTGVNMLSPGESEHLLEPAEAERSORRRLLVPANEGDPTE 307
     7.1%; Score 192; DB 4; Length 471;
                                                                                      Query Match 7.1%; Score 192; DB 4; L
Best Local Similarity 34.6%; Pred. No. 3.21e-14;
                                                                                      Matches 36: Conservative 16: Mismatches 41: Indels 11: Gaps 10:
RESULT 8
                                                                                           70 NDCP-GPGR-D-TD-CRVCAPGT-YTALENHLRRCLSCSRCRDEMFOVEISPCVVDRDTV 124
ID 000220
                PRELIMINARY: PRT: 468 AA.
                                                                                           AC 000220;
   01-JUL-1997 (TREMBLREL, 04, CREATED)
   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                          125 CGCRKNOVERYWGETGERCLNCSL-CPNGTVNIP-COERODTIC 166
                                                                                          DE CYTOTOXIC LIGAND TRAIL RECEPTOR.
OS HOMO SAPIENS (HUMAN).
    EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
00
OC
    EUTHERIA: PRIMATES.
                                                                                    RESULT 10
                                                                                    ID 062327
                                                                                                      PRELIMINARY; PRT; 459 AA.
RN
RP
    SECUENCE FROM N.A.
RX
    MEDLINE: 97238921.
                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
    PAN G., O'ROURKE K., CHINNAIYAN A.M., GENTZ R., EBNER R., NI J.,
                                                                                         01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
   DIXIT V.M.:
    SCIENCE 276:111-113(1997).
    EMBL; U90875; G1945072; -.
                                                                                         TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
   SEQUENCE 468 AA: 50025 MW: 95AEFC6F CRC32:
                                                                                         MUS MUSCULUS (MOUSE).
                                                                                     OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                     28.9%; Score 784; DB 2; Length 468;
                                                                                     OC.
                                                                                         EUTHERIA: RODENTIA.
 Best Local Similarity 48.8%; Pred. No. 1.06e-128;
Matches 168; Conservative 60; Mismatches 79; Indels 37; Gaps 19;
                                                                                    RN
                                                                                         [1]
                                                                                    RP
                                                                                         SEQUENCE FROM N.A.
                                                                                     RC STRAIN=NOD:
      60 GOHGPSAR-ARAGRAPGPRPAREASPRLRVHKTFKFVV--VGVLLOV-VPSSAATIK--L 113
                                                                                    RX MEDLINE: 95178848.
       POWELL E.E., WICKER L.S., PETERSON L.B., TODD J.A.;
                                                                                     RA
                                                                                    RL MAMM. GENOME 5:726-727(1994).
                                                                                     DR EMBL: X76401: G433831: *.
                                                                                     DR PROSITE; PS00652; TNFR_NGFR 1: 2.
     114 HDOSIGTOOWEHSPL-GELCPPGSHRSERPGACNRCTEGVGYTNASNNLFACLPCTACKS 172
          aleas il as ar a marrino mor mor or mor an in inci-
                                                                                    FT
                                                                                         NON TER
      65 POOTVAPOO-ORRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLICTVCKS 123
                                                                                         VARTANT
                                                                                         VARIANT
                                                                                                   93 93
                                                                                                                 T -> T.
                                                                                                   268 268
345 345
421 421
     173 DEEERS POTTENTACOCK POTFENDINS A EMCRKOST GCPROMVKVK DCTPWSD I ECVHK 232
                                                                                     PT
                                                                                         VARIANT
                                                                                                                  F -> I.
         a eleminat di Tale nami i munkiti amani la
                                                                                     FΤ
                                                                                         VARTANT
                                                                                                                  S -> F
     124 COTINGSCOTTER DEVOCCERCISEODE INSPERIOR TORT GORGAVICA SUCTORS DIRECTOR 183
                                                                                    FT VARIANT
                                                                                                                   Y -> C.
                                                                                     SO SEQUENCE 459 AA: 48686 MW; 57791809 CRC32;
     233 -- ES--GN---GHN-IWVIL-VVT-----LVVPLLLVAVL--IVC--CC----IG--SG- 267
           7.0%; Score 191; DB 10; Length 459;
                                                                                      Best Local Similarity 27.6%; Pred. No. 4.71e-14;
Matches 29; Conservative 27; Mismatches 44; Indels 5; Gaps 5;
     184 SAASSTCKTPAAEETVTTILGMLASPYHYLIIIVVLVIILAVVVVGFSCRKKFISYLKGI 243
     268 C---GGDPKCMDRVCFWRLG-LLRGPGAEDNAHNEILSNADSLSTFVSEOOMESQEPADL 323
Db
                                                                                           61 CADCEASM-YTOVWNOFRTCLSCSSSCSTDOVETRACTKOONRVCACEAGRYCALKTHSG 119
        244 CSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLOPTOVSEOEIOGOELAEL 303
     324 TGVTVOSPGRAOCILIGPARAEGSORRRILLVPANGADPTETIMUF 367
                                                                                          120 SCROCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTD 164
         DOBET BELLE BOLDOOD I BEEL DE
     304 TGVTVEXPEEPORLLEQAEAEGCORRRLLVPVNDADSADISTLL 347
                                                                                              154 MCRTC-RTG-CPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAE 196
RESULT 9
ID 019131
                PRELIMINARY; PRT; 471 AA.
                                                                                    RESULT 11
                                                                                     ID 085407
                                                                                                      PRELIMINARY; PRT; 348 AA.
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                     DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                         01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE TUMOR NECROSIS FACTOR-RECEPTOR I.
                                                                                         01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                     DE HOMOLOG OF VACCINIA VIRUS CDS B28R.
GN TNF-RI.
OS BOS TAURUS (BOVINE).
                                                                                     CN
   EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
                                                                                     0S
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VIRIDAE: DS-DNA ENVELOPED VIRUSES: POXVIRIDAE: CHORDOPOXVIRINAE;

RC STRAIN=SOMALIA-1977:

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OC ORTHOPOXVIRUSES.
                                                                                                                                                                                     RA MASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,
                                                                                                                                                                                     RA TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;
         [1]
         SECUENCE FROM N.A.
                                                                                                                                                                                              SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
RC STRAIN=BANGLADESH-1975;
                                                                                                                                                                                     DR EMBL; U18341; G885855; -.
         MEDLINE: 94088747.
                                                                                                                                                                                     DR PROSITE; PS00652; TNFR_NGFR_1; 2.
         MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
                                                                                                                                                                                     SO SEQUENCE 349 AA: 38272 MW; OFDCC784 CRC32;
         KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;
         NATURE 366:748-751(1993).
                                                                                                                                                                                                                                       6.9%; Score 187; DB 11; Length 349;
DR EMBL; L22579; G439102; -
                                                                                                                                                                                         Best Local Similarity 37.1%; Pred. No. 2.16e-13;
         PROSITE; PS00652; TNFR_NGFR_1; 2.
                                                                                                                                                                                         Matches 33; Conservative 18; Mismatches 31; Indels 7; Gaps 6;
SQ SEQUENCE 348 AA; 38075 MW; 2A911AF6 CRC32;
                                                                                                                                                                                                   65 CTPCGSGT-FTSRNNHLPACLSCNGRCNSNOVETRSCNTTHNRICECSPGYYCLLKGSSG 123
                                                                                                                                                                                                  6.9%; Score 187; DB 11; Length 348;
   Best Local Similarity 37.1%; Pred. No. 2.16e-13;
Matches 33; Conservative 18; Mismatches 31; Indels 7; Gaps 6;
                                                                                                                                                                                                124 -CKACVSQTKCGIGYG-VSGHTSVGDVIC 150
             64 CTPCGSGT-FTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSG 122
                                                                                                                                                                                                          1:1:1:11 1 1::1:1
             | | | | : | : | : | | : | | : | | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                154 MCRTC -- RTGCPRGMVKVSNCTPRSDIKC 180
           123 -CKACVSOTKCGIGYG-VSGHTSVGDVIC 149
           |::| :| | | | | |: :|: |
154 MCRTC--RTGCPRGMYKVSNCTPRSDIKC 180
                                                                                                                                                                                      ID 085308
                                                                                                                                                                                                                            PRELIMINARY: PRT: 355 AA.
                                                                                                                                                                                     AC 085308:
                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                              01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
ID Q89098
                                      PRELIMINARY; PRT; 349 AA.
                                                                                                                                                                                              SECRETED RECEPTOR BINDING TUMOR NECROSIS FACTOR (CRMB).
         nganag.
                                                                                                                                                                                     GN
                                                                                                                                                                                               CRMR
         01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                               COWPOX VIRUS (CPV).
         01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
                                                                                                                                                                                               VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
         01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                              ORTHOPOXVIRUSES.
         GARCIA-1966 RIGHT NEAR-TERMINAL REGION.
                                                                                                                                                                                     RN
                                                                                                                                                                                               [1]
         VARIOLA VIRUS.
                                                                                                                                                                                     RP
                                                                                                                                                                                               SEQUENCE FROM N.A.
         VIRIDAE: DS-DNA ENVELOPED VIRUSES: POXVIRIDAE: CHORDOPOXVIRINAE:
                                                                                                                                                                                              STRAIN-BRIGHTON RED:
         ORTHOPOXVIRUSES.
                                                                                                                                                                                               MEDLINE: 83117629.
         [1]
                                                                                                                                                                                               PICKUP D.J., BASTIA D., STONE H.O., JOKLIK W.K.;
                                                                                                                                                                                               PROC. NATL. ACAD. SCI. U.S.A. 79:7112-7116(1982).
RP
         SECUENCE FROM N.A.
         STRAIN-GARCIA-1966:
         MASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,
                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                      RP
         TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;
                                                                                                                                                                                     יאמ
                                                                                                                                                                                              STRAIN-BRIGHTON RED;
         SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                              MEDLINE; 90177240.
DR EMBL; U18339; G885793; ...
                                                                                                                                                                                              PARSONS B.L., PICKUP D.J.;
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
                                                                                                                                                                                               VIROLOGY 175:69-80(1990).
SQ SEQUENCE 349 AA; 38262 MW; C9A42899 CRC32;
                                                                                                                                                                                      RN
                                                                                                                                                                                      ВÞ
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                 6.9%; Score 187; DB 11; Length 349;
                                                                                                                                                                                            STRAIN-BRIGHTON RED:
   Best Local Similarity 37.1%; Pred. No. 2.16e-13;
Matches 33; Conservative 18; Mismatches 31; Indels 7; Gaps 6;
                                                                                                                                                                                     RX MEDLINE: 91196263.
                                                                                                                                                                                     RA
                                                                                                                                                                                              HU F.Q., PICKUP D.J.;
                                                                                                                                                                                     RI.
                                                                                                                                                                                               VIROLOGY 181:716-720(1991).
             65 CTPCGSGT-FTSRNNHLPACLSCNGRCNSNOVETRSCNTTHNRICECSPGYYCLLKGSSG 123
                                                                                                                                                                                              SEQUENCE FROM N.A.
             рp
                                                                                                                                                                                               STRAIN-BRIGHTON RED:
                                                                                                                                                                                              MEDLINE; 94378510.
                                                                                                                                                                                              HU F.Q., SMITH C.A., PICKUP D.J.;
           124 -CKACVSOTKCGIGYG-VSGHTSVGDVIC 150
                                                                                                                                                                                              VIROLOGY 204:343-356(1994).
                     161 311 1 11 16 16 1
           154 MCRTC - RTGCPRGMVKVSNCTPRSDIKC 180
                                                                                                                                                                                              EMBL; L08906; G333519; -.
                                                                                                                                                                                     SO SEQUENCE 355 AA: 39008 MW: 8A40AAAE CRC32:
RESULT 13
                                                                                                                                                                                                                                      6.9%; Score 186; DB 11; Length 355;
                                                                                                                                                                                         Best Local Similarity 32.6%; Pred. No. 3.16e-13;
ID 089118
                                      PRELIMINARY; PRT; 349 AA.
                                                                                                                                                                                         Matches 31; Conservative 22; Mismatches 37; Indels 5; Gaps 4;
         01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                  58 KININTOCIPCASDI-FISRNNHLPACLSCNGRCDSNOVETRSCNITHNRICDCAPGYYC 116
         01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL, 05, LAST ANNOTATION UPDATE)
         SOMALIA-1977 RIGHT NEAR-TERMINAL REGION.
         SHALL VIOLARA
                                                                                                                                                                                                117 FLKGSSGCKACVSOTKCGIGYG-VSGHTPTGDVVC 150
         VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                            and the late of th
                                                                                                                                                                                                 148 DKNSPEMCRTC -- RTGCPRGMVKVSNCTPRSDIKC 180
OC.
         ORTHOPOXVIRUSES.
RN
         [1]
        SEQUENCE FROM N.A.
```

RESULT 15

```
ID Q14293
                   PRELIMINARY; PRT; 314 AA.
AC Q14293;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE FAS SOLUBLE PROTEIN.
     HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN
     [1]
RP
     SEQUENCE FROM N.A.
RX MEDLINE; 95181785.
RA CASCINO I., FIUCCI G., PAPOFF G., RUBERTI G.;
RL J. IMMUNOL. 154:2706-2713(1995).
DR EMBL; 247993; G695539; -.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
SQ SEQUENCE 314 AA; 35386 MW; F39D50D5 CRC32;
                         6.7%; Score 182; DB 2; Length 314;
  Best Local Similarity 35.6%; Pred. No. 1.44e-12;
  Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;
       82 CVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVCE 141
         difficil e el la le entière de l
```

96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGQT-N-KSSCTTTRDTVCQCEKGSFQDKNSPE 153

142 HCDPC-TKCEHGIIK--ECTLTSNTKCKEE 168 1 1 1 1 3 3 3 3 1 3 1 1 1 1 1 1 1 154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNE 183

Db

e 18.3

Search completed: Thu May 14 16:49:06 1998 Job time : 52 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:50:10 1998; MasPar time 11.05 Seconds 522.069 Million cell updates/sec

Tabular output not generated.

>US-08-918-874-1 Title:

Description: (1-386) from US08918874.pep

Perfect Score: 2715

Sequence: 1 MGLWGQSVPTASSARAGRYP......VGSEKLFYEEDEAGSATSCL 386

Scoring table: PAM 150

Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%

8

Listing first 45 summaries

Database: a-geneseg31

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23

24:part24 25:part25 26:part26

Statistics: Mean 34.398; Variance 153.278; scale 0.224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description	Pred. No.
1	201	7.4	600 14	R78610	Expression vector pME	1.65e-07
2	195	7.2		R11142	TNF-R deduced from mT	5.19e-07
3	191	7.0	335 5	R28084	Human cell surface an	1.11e-06
4	191	7.0	335 14	R78606	Human Fas protein.	1.11e-06
5	191	7.0	335 17	R92528	hFas from plasmid pCE	1.11e-06
6	191	7.0	335 18	R99681	Human Fas antigen.	1.11e-06
7	186	6.9	355 15	R85073	Cowpox virus T2-equiv	2.87e-06
8	188	6.9	592 17	R92527	Fas antigen #2.	1.97e-06
9	187	6.9	600 17	R92526	Fas antigen #1.	2.38e-06
10	184	6.8	576 14	R78613	Expression vector pME	4.19e-06
11	182	6.7	314 18		Human Fas soluble ant	6.12e-06
12	182	6.7	314 13		Fas-delta-TM.	
13	179	6.6	159 4		Truncated TNF-alpha 5	1.08e-05
14	180	6.6	326 5	R27866	Myxoma virus T2 prote	8.91e-06
15	180	6.6		R85072	Myxoma virus T2 prote	8.91e-06
16	177	6.5		R78612	Plasmid fragment pME1	1.57e-05
17	176	6.5	285 26	W33359	TBP(20-190)/hCG-a1pha	1.89e-05
18	177	6.5		R92530	mFas sequence.	
19 ·	177	6.5	327 14	R78611	Murine Fas antigen ex	1.57e-05

20	177	6.5	327	8	R41688	Murine Fas.	1.57e-05
21	173	6.4	161	5	R27496	Native 30 kD TNF inhi	3.31e-05
22	173	6.4	168	4	R24084	Truncated TNF-alpha 5	3.31e-05
23	173	6.4	199	4	R24080	Truncated TNF-alpha 5	3.31e-05
24	173	6.4	256	26	W33357	TBP(20-161)/hCG-alpha	3.31e-05
25	173	6.4	307	26	W33358	TBP(20-161)/hCG-beta	3.31e-05
26	173	6.4	309	13	R70108	TNF-R-GBPH fusion pro	3.31e-05
27	173	6.4	336	26	W33360	TBP(20-190)/hCG-beta	3.31e-05
28	173	6.4	371	2	R07449	Tumour Necrosis Facto	3.31e-05
29	173	6.4	451	13	R70107	TNF-R-GBP 130 fusion	3.31e-05
30	173	6.4	455	14	R75084	p55 TNF-R.	3.31e-05
31	173	6.4	455	4	R24000	TNF-alpha 55kD recept	3.31e-05
32	173	6.4	455	2	R11082	Human 55kD TNF-bindin	3.31e-05
33	173	6.4	455	2	R07451	Human Tumour Necrosis	3.31e-05
34	173	6.4	455	2	R10986	30kD TNF inhibitor pr	3.31e-05
35	173	6.4	455	3	R12550	Type I TNF receptor.	3.31e-05
36	173	6.4	455	8	R42059	Lambda derived TNF-R.	3.31e-05
37	173	6.4	455	4	R20787	TNF-alpha binding pro	3.31e-05
38	173	6.4	547	13	R70104	TNF-R-GBPH fusion pro	3.31e-05
39	173	6.4	884		R70109	TNF-R-GBP 130 fusion	3.31e-05
40	173	6.4	900	13	R70103	TNF-R-GBP 130 fusion	3.31e-05
41	173	6.4	1245	13	R70106	TNF-R-Pl. vivax Duffy	3.31e-05
42	173	6.4	1604	13	R70105	TNF-R-EBA 175 fusion	3.31e-05
43	167	6.2	393	20	R99948	Mutated OCIF, OCIF-CB	1.01e-04
44	167	6.2	399	20	R99942	Mutated OCIF, OCIF-CL	1.01e-04
45	169	6.2	401	20	R99933	Mutated OCIF, OCIF-C2	6.97e-05

ALIGNMENTS

RESU	LT 1	
ID	R78610 standard	; Protein; 600 AA.
AC	R78610;	
DΤ	19-FEB-1996 (f	irst entry)
DE	Expression vect	or pME18S/hFas.EXT-AIC2A protein prod
K₩	Expression vect	or; pME18S/hFas.EXT-AIC2A; human Fas antigen;
K₩	extracellular;	region; AIC2A; soluble membrane protein;
K₩	antibody produc	tion; diseases; treatment; prevention.
0S	Homo sapiens.	•
FH	Key	Location/Qualifiers
ΡT	peptide	116
PT		/label= sig_peptide
FT	peptide	17600
ΡT		/label= mat_peptide
PN	J07115988-A.	
PD	09-MAY-1995.	
PF	26-OCT-1993; 26	7644.
PR	26-OCT-1993; JP	-267644.
PA	(NISB) JAPAN T	OBACCO INC.
DR	WPI; 95-202847/	27.
DR	N-PSDB; Q95301.	
PΤ	Preparation of	soluble membrane proteins - for their use in antibody
PΤ	production for	the treatment and prevention of related diseases
PS		28-30; 51pp; Japanese.
CC		rotein prod. of the expression vector pME18S/human Fas
CC		llular region-AIC2A. The expression vector was used for
CC		ecombinant soluble membrane proteins. The proteins can

diseases.

be used in antibody prodn. for the treatment and prevention of related

Sequence 600 AA;

7.4%; Score 201; DB 14; Length 600; Query Match Best Local Similarity 35.8%; Pred. No. 1.65e-07;
Matches 38; Conservative 22; Mismatches 40; Indels 6; Gaps 5;

82 cvpcqegkeytdkahfsskcrrcrlcdeghgleveinctrtqntkcrckpnffcnstvce 141 96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGOT-N-KSSCTTTRDTVCQCEKGSFQDKNSPE 153

142 hcdpc-tkcehqiik--ectltsntkckeeqsrsvaavt-eeeetv 183

154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETV 199

P?

```
RESULT 2
ID R11142 standard; Protein; 474 AA.
         R11142;
         24-MAY-1991 (first entry)
         TNF-R deduced from mTNF-R clone 11.
        Tumour necrosis factor receptor; immune response; inflammation;
         cachexia; septic shock.
OS
         Mus musculus strain C57BL/6.
PH
         Key
                                        Location/Qualifiers
FT peptide
                                        1..22
                                         /label= signal sequence
PT
ΡŦ
                                         234..265
                                        /label= transmembrane region
         EP-418014-A.
         20-MAR-1991
PΠ
PF
         10-SEP-1990; 309875.
         11-SEP-1989: US-405370
         13-OCT-1989: US-421417.
          10-MAY-1990: US-523635.
         (IMMU-) IMMUNEX CORP.
         Smith CA. Goodwin RG. Beckmann PM:
         WPI; 91-082230/12.
DR
         New tumour necrosis factor -alpha and -beta receptors - and DNA
         encoding these used to regulate immune responses in treatment of
         cachexia, septic shock or side-effects of cytokine therapy.
         Disclosure; Fig 3; 41pp; English.
         The sequence was deduced from a clone isolated from library prepd.
         from a murine T helper cell line, 7B9.
         See also R11141.
SQ Sequence 474 AA;
                                                  7.2%; Score 195; DB 2; Length 474;
    Best Local Similarity 28.6%; Pred. No. 5.19e-07;
   Matches 30; Conservative 27; Mismatches 43; Indels 5; Gaps 5;
              76 cadceasm-ytqvwnqfrtclscssscttdqveiractkqqnrvcaceagrycdlkthsg 134
             | | | :: | | | | : : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
           135 scrqcmrlskcgpgfgvassrapngnvlckacapgtfsdttsstd 179
          RESULT 3
ID R28084 standard; Protein; 335 AA.
         12-MAR-1993 (first entry)
         Human cell surface antigen.
         Fas antigen; apoptosis; pF58; NGFR/TNFR family.
OS
         Homo sapiens.
FΗ
          Key
                                          Location/Qualifiers
ΡT
         peptide
                                         1 16
                                         /label= signal
                                         17...335
ΡĪ
         protein
                                         /label= Fas_antigen
         modified_site 118..120
                                         /label= N-glycosylation site
                                         /note= 'putative'
FT
FT
         modified_site 136..138
                                         /label= N-glycosylation_site
FT
                                         /note= "putative"
         domain
                                         174...190
                                         /label= transmembrane
FT
         domain
                                         17...173
                                         /label= extracellular
                                          /note= "cysteine-rich"
                                          191..335
PT
        domain
                                         /label= cytoplasmic
PN EP-510691-A.
PD 28-0CT-1992.
```

```
PF 24-APR-1992: 107060
    26-APR-1991; JP-125234.
PR
PΑ
    (OSAB-) OSAKA BIOSCIENCE INST.
    Itoh N. Nagata S. Yonehara S:
PΤ
    WPI: 92-358914/44.
DR
    N-PSDB: 029959.
    DNA encoding human cell surface antigen - used to clarify
    apoptosis mechanism of various types of cell, and to prepare
PΨ
    monoclonal antibodies that react with tumour cells expressing Fas
    Claim 3: Fig 1 and 2; 27pp; English.
CC The Fas antigen is implicated in apoptosis. A cDNA clone encoding
    the antigen was isolated (pF58) and the amino acid sequence of Fas
    was deduced from it. The mature protein has a calculated mol.wt. of
   36,000 and is a member of the NGFR/TNFR family of cell-surface
CC membrane proteins. The inventors claim a protein comprising at
   least the extracellular domain of Fas antigen.
SQ Sequence 335 AA;
 Query Match 7.0%; Score 191; DB 5; Length 335; Best Local Similarity 35.1%; Pred. No. 1.11e-06; Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;
      82 cvpcqeqkeytdkahfsskcrrcrlcdeghgleveinctrtqntkcrckpnffcnstvce 141
         96 CNPCTEGVDYTIASNNIPSCLLCTVCKSGOT-N-KSSCTTTRDTVCOCEKGSFODKNSPE 153
     142 hcdpc-tkcehgiik--ectltsntkckeegsrsnlg 175
          4 î.H. Haish all Ta 116 îs 1a î
     154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTG 190
RESULT 4
ID R78606 standard; Protein; 335 AA.
DT
    19-FEB-1996 (first entry)
DE Human Pas protein.
KW Plasmid pF58; human Fas cDNA; soluble membrane protein;
    antibody production; diseases; treatment; prevention.
KW
OS
    Homo sapiens.
FH
                    Location/Oualifiers
    Key
ΡT
    peptide
                   1..16
                    /label= sig_peptide
FΤ
    peptide
                    17 335
                    /label= mat_peptide
    лот115988-а.
PN
PD
    09-MAY-1995.
    26-OCT-1993; 267644.
PF
    26-OCT-1993; JP-267644
PA
    (NISB ) JAPAN TOBACCO INC.
WPI: 95-202847/27.
DR
    N-PSDB: 095297.
    Preparation of soluble membrane proteins - for their use in antibody
    production for the treatment and prevention of related diseases
    Example 1; Pages 15-17; 51pp; Japanese.
    R78606 (human Fas protein) is encoded by the plasmid pF58 which
    contains hFas cDNA. The plasmid was used in the construction of an
    expression vector for the prodp. of recombinant soluble membrane
    proteins. The proteins can be used in antibody prodn. for the
    treatment and prevention of related diseases.
SQ Sequence 335 AA;
                        7.0%; Score 191; DB 14; Length 335;
 Best Local Similarity 35.1%; Pred. No. 1.11e-06;
 Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;
      82 cvpcqeqkeytdkahfsskcrrcrlcdeqhqleveinctrtqntkcrckpnffcnstvce 141
      142 hcdpc·tkcehqiik·-ectltsntkckeegsrsnlg 175
         154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTG 190
```

PN W09620206-Al.

```
RESULT 5
ID R92528 standard; Protein; 335 AA.
   R92528:
    06-SEP-1996 (first entry)
     hFas from plasmid pCEV4/hFas.
KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW rheumatoid arthritis; serum; systemic lupus erythematosus.
FH Key
                     Location/Oualifiers
FT peptide
                     1..16
                     /note= "hFas signal peptide"
    protein
                     17 335
                     /note= "mature hPas"
PN W09601277-A1.
PD 18-JAN-1996.
PF 03-MAR-1995; J00349.
     06-JUL-1994: JP-154706
PR 14-PEB-1995: JP-025637.
   (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
    (NISB ) JAPAN TORACCO INC.
     Hachiya T, Noguchi J, Yonehara S;
DR WPI: 96-087635/09.
     N-PSDB; T16303.
     Immunoassay method for soluble Fas antigen in body fluids - for
     diagnosis of auto:immune diseases such as rheumatoid arthritis and
    systemic lupus erythematosus
     Example 8; Page 49-52; 124pp; Japanese.
    This sequence represents the sequence for the human Fas antigen contained
    within the plasmid pCEV4/hFas. The soluble Fas antigen is included in
the immunoassay kit of the invention. The kit is for the assay of
    soluble Fas antigen and contains an immobilised anti-soluble Fas
    monoclonal antibody, as well as the standard soluble Fas antigen
    represented by this sequence. The assay is simple and has high accuracy,
     high sensitivity, and is capable of assaying a number of different
    specimens at the same time. The immunoassay is used on biological
     samples (such as serum) and is useful for diagnosis of autoimmune
CC diseases such as rheumatoid arthritis or systemic lupus erythematosus
SQ Sequence 335 AA:
                         7.0%; Score 191; DB 17; Length 335;
  Best Local Similarity 35.1%; Pred. No. 1.11e-06;
  Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;
       82 cvpcqegkeytdkahfsskcrrcrlcdeqhqleveinctrtqntkcrckpnffcnstvce 141
          Tirliair a a r Earlia a niarm i na T
       96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGOT-N-KSSCTTTRDTVCOCEKGSFODKNSPE 153
Q٧
     142 hcdpc-tkcehgiik--ectltsntkckeegsrsnlg 175
          at i fat taist an teamsis tei
      154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTG 190
RESULT 6
ID R99681 standard: Protein: 335 AA.
   R99681:
    10-OCT-1996 (first entry)
     Human Pas antigen.
     Fas antiqen; autoimmune disease; systemic lupus erythematosus; SLE;
    angioimmunoblastic lymphadenopathy; AILD.
     Homo sapiens.
FH Key
                     Location/Qualifiers
PΤ
    peptide
                     1..16
                     /label= Sig_peptide
   protein
                     17...335
                     /label= Mat protein
    domain
                     17...173
                     /label= Extracellular domain
FT domain
                     174 190
                     /label= Transmembrane domain
FT domain
                     191..335
                    /label= Cytoplasmic_tail
```

```
04-JUL-1996.
PD
        22-DEC-1995: U17083
PF
        23-DEC-1994: US-371263
        (UABR-) UAB RES FOUND.
        Cheng J, Liu C, Mountz JD, Zhou T;
        WPI: 96-321796/32.
        Natural, soluble form of Fas antigen secreted by human cells is
        result of alternative mRNA processing - used to diagnose
        Fas-associated disease, e.g. systemic lupus erythematosus
        Disclosure: Page 109-111: 152pp; English.
        A cDNA clone (T34526) codes for a membrane receptor-like protein,
        Fas antigen (R99681). It was isolated from cDNA derived from the
        peripheral blood mononuclear cells of systemic lupus erythematosus
        (SLE) and angicimmunoblastic lymphadenopathy (AILD) patients. 4
        Soluble variants (R99682-85) were identified of the Fas antigen.
        These arose by alternative splicing of Fas gene transscripts. The
        Fas variants were present at higher levels in SLE and AILD patients
        than the non-soluble Fas antigen.
SQ Sequence 335 AA;
   Query Match
                                            7.0%; Score 191; DB 18; Length 335;
    Best Local Similarity 35.1%; Pred. No. 1.11e-06;
   Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;
             82 cvpcqeqkeytdkahfsskcrrcrlcdeghgleveinctrtgntkcrckpnffcnstvce 141
            142 hcdpc-tkcehqiik--ectltsntkckeeqsrsnlq 175
                 ori i i i distori di distillatis dell
          154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTG 190
        R85073 standard: Protein: 355 AA.
        R85073;
        16-APR-1996 (first entry)
        Cowpox virus 72-equivalent protein.
        Cowpox virus; immunosuppressive; cytokine antagonist;
        tumour necrosis factor antagonist; therapeutic; cachexia;
        septic shock.
        Cowpox virus.
20
        US5464938-A.
        07-NOV-1995.
        18-AUG-1994: 292549.
        19-OCT-1992: US-963330.
        (IMMV ) Immunex Corp.
        Goodwin RG, Smith CA
        WPI: 95-402861/51.
        N-PSDB: T02472.
        New soluble viral proteins that bind tumour necrosis factor - for
        treating cachexia, septic shock, side effects of TNP therapy etc.,
        also useful in assays, affinity purificm. and antibody prodm.
        Claim 1; Columns 35-38; 21pp; English.
        The cowpox virus T2-equivalent protein is a soluble viral protein
        which binds tumour necrosis factor (TNF), thus inhibiting TNF
        binding to its receptor. T2 protein is useful (when administered
        by injection or infusion from sustained release implants, etc.) for
        treating TNF associated toxicity e.g. side effects of using TNF as
        an antitumour agent or in cases of cachexia and septic shock where
        TNF production is excessive.
SQ Sequence 355 AA;
                                             6.9%; Score 186; DB 15; Length 355;
   Best Local Similarity 32.6%; Pred. No. 2.87e-06;
Matches 31; Conservative 22; Mismatches 37; Indels 5; Gaps 4;
            58 ktntntqctpcasdt-ftsrnnhlpaclscngrcdsnqvetrscntthnricdcapgyyc 116
            ::: | ||: :|:||| | | | | : | | ||:::|| | : | | | : | | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
```

```
117 flkgssgckacvsqtkcgigyg-vsghtptgdvvc 150
     ::: |::| :| | | | | | | :|: |

148 DKNSPPMCPTC--RTGCPRGMVKVSNCTPRSDIKC 180
ID R92527 standard; Protein; 592 AA.
    R92527:
    06-SEP-1996 (first entry)
    Fas antigen #2.
    Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
    rheumatoid arthritis; serum; systemic lupus erythematosus.
    Synthetic.
    Key
                    Location/Qualifiers
    peptide
                    1..21
FT
FT
                    /note= "signal peptide"
                    22...592
    protein
                    /note= "mature Fas antigen #2"
    W09601277-A1.
    18-JAN-1996.
    03-MAR-1995: J00349.
    06-JUL-1994; JP-154706.
    14-FER-1995: JP-025637
    (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
    (NISB ) JAPAN TOBACCO INC.
    Hachiva T, Noguchi J, Yonehara S;
    WPI: 96-087635/09.
    N-PSDB: T16301.
    Immunoassay method for soluble Fas antigen in body fluids - for
    diagnosis of auto:immune diseases such as rheumatoid arthritis and
    systemic lupus erythematosus
    Claim 11: Page 87-91; 124pp; Japanese.
    R92526 and R92527 represent soluble Fas antigens. These soluble Fas
    antigen is included in the immunoassay kit of the invention. The kit is
    for the assay of soluble Fas antigen and contains an immobilised
    anti-soluble Fas monoclonal antibody, as well as one of these standard
    soluble Fas antigens. The assay is simple and has high accuracy, high
    sensitivity, and is capable of assaying a number of different specimens
    at the same time. The immunoassay is used on biological samples (such as
    serum) and is useful for diagnosis of autoimmune diseases such as
CC rheumatoid arthritis or systemic lupus erythematosus (SLE).
SO Sequence 592 AA;
                        6.9%; Score 188; DB 17; Length 592;
 Query Match
 Best Local Similarity 31.8%; Pred. No. 1.97e-06;
  Matches 35; Conservative 26; Mismatches 42; Indels 7; Gaps 7;
      75 tptcapctegkey-mdknhypdkcrrctlcdeehglevetnctltgntkckckpdfycds 133
      134 pgcehcvrc-ascehgtle-p-ctatsntncrkgsprnrlwhvteeeetv 180
          ši i i i selača ži Baladešča i
     150 NSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETV 199
    R92526 standard: Protein: 600 AA.
    R92526;
    06-SEP-1996 (first entry)
    Fas antigen #1.
    Fas: antigen: immunoassav: monoclonal antibody; autoimmune disease; SLE;
    rheumatoid arthritis; serum; systemic lupus erythematosus.
    Synthetic.
                    Location/Qualifiers
    peptide
FT
                    1..16
                    /note= "signal peptide"
    protein
                    17..600
                    /note= "mature Fas antigen #1"
PN W09601277-A1.
    18-JAN-1996.
    03-MAR-1995; J00349.
PR 06-JUL-1994; JP-154706.
```

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PR 14-PEB-1995; JP-025637.
    (MEDI*) MEDICAL & BIOLOGICAL LAB CO LTD.
    (NISB ) JAPAN TOBACCO INC.
PΙ
    Hachiya T, Noguchi J, Yonehara S;
    WPI: 96-087635/09.
    N-PSDB: T16300.
    Immunoassay method for soluble Fas antigen in body fluids - for
    diagnosis of auto:immune diseases such as rheumatoid arthritis and
PΤ
    systemic lupus erythematosus
    Claim 13; Page 73-77; 124pp; Japanese.
    R92526 and R92527 represent soluble Fas antigens. These soluble Fas
    antigen is included in the immunoassay kit of the invention. The kit is
    for the assay of soluble Fas antigen and contains an immobilised
    anti-soluble Fas monoclonal antibody, as well as one of these standard
    soluble Fas antigens. The assay is simple and has high accuracy, high
    sensitivity, and is capable of assaying a number of different specimens
    at the same time. The immunoassay is used on biological samples (such as
    serum) and is useful for diagnosis of autoimmune diseases such as
    rheumatoid arthritis or systemic lupus erythematosus (SLE).
SO Sequence 600 AA;
 Query Match 6.9%; Score 187; DB 17; Length 600; Best Local Similarity 34.9%; Pred. No. 2.38e-06;
 Matches 37; Conservative 22; Mismatches 41; Indels 6; Gaps 5;
       82 cvpsqeqkeytdkahfsskcrrcrlcdeghgleveinctrtqntkcrckpnffcnstvce 141
      142 hcdpc-tkcehgiik--ectltsntkckeegsrsvaavt-eeeetv 183
          154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETV 199
RESULT 10
TD R78613 standard: Protein: 576 AA.
    R78613 ·
     20-FEB-1996 (first entry)
    Expression vector pME18S/mFas.EXT-AIC2A protein prod..
DE
    Expression vector; pME18S/mFas.EXT-AIC2A; murine Fas antigen;
    extracellular; region; AIC2A; soluble membrane protein;
    antibody production; diseases; treatment; prevention.
Λ¢
    Mus musculus.
    J07115988-A.
    09-MAY-1995.
חם
    26-OCT-1993: 267644.
    26-007-1993: JP-267644.
    (NISB ) JAPAN TOBACCO INC.
     WPI: 95-202847/27.
D.P.
    N-PSDB: 095306.
    Preparation of soluble membrane proteins - for their use in antibody
    production for the treatment and prevention of related diseases
     Claim 10: Pages 36-38; 51pp; Japanese.
    R78613 is the protein prod. of the expression vector pME18S/murine Fas
    antigen.extracellular region-AIC2A. The expression vector was used for
     the prodn. of recombinant soluble membrane proteins. The proteins can
    he used in antihody produ. for the treatment and prevention of related
    diseases
SO Sequence 576 AA;
 Query Match 6.8%; Score 184; DB 14; Length 576; Best Local Similarity 30.3%; Pred. No. 4.19e-06;
 Matches 33; Conservative 26; Mismatches 45; Indels 5; Gaps 5;
       75 tptcapctegkeymdknhyadkcrrctlcdeehglevetnctltqntkckckpdfycdsp 134
      135 gcehcvrc-ascehgtle-p-ctatsntncrkqsprnrlwhvteeeetv 180
```

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RESULT 11
                                                                                                            Location/Oualifiers
ID R99682 standard: Protein: 314 AA.
                                                                                             peptide
                                                                                        FT
                                                                                                            1..16
AC R99682;
                                                                                        FT
                                                                                                            /label= Sig_peptide
DT 10-OCT-1996 (first entry)
                                                                                             W09513701-A.
                                                                                        PN
DE Human Fas soluble antigen Fas dell.
                                                                                             26-MAY-1995.
    Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
                                                                                             15-NOV-1994; U13173.
    angioimmunoblastic lymphadenopathy; AILD.
                                                                                             15-NOV-1993: US-152443.
    Homo sapiens.
                                                                                        PA (LXRB-) LXR BIOTECHNOLOGY INC.
FH Key
                    Location/Qualifiers
                                                                                             Barr PJ, Kiefer MC, Shapiro JP;
FT peptide
                   1..16
                                                                                             WPI: 95-200120/26.
                                                                                        DR
                    /label= Sig_peptide
                                                                                        DR
                                                                                             N-PSDB: 093879.
ΡŦ
    protein
                   17...314
                                                                                             New nucleic acid encoding Fas protein without its trans-membrane region
FT
                    /label= Mat protein
                                                                                             - and related vectors, transformed cells, transgenic animals, protein and
                    /note= "soluble Fas dell antigen"
                                                                                             antibodies, useful for control of Fas mediated apoptosis
                    17..168
    domain
                                                                                             Claim 9: Fig.3-1 to 3-4: 38pp: English.
                    /label= Extracellular domain
                                                                                             mRNA was obtd. from human lymphocytes and PCR was used to make
FT
                    /note= "the 5 C-terminal residues of the
                                                                                             cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
FT
                    Fas antigen extracellular domain are
                                                                                             region) mRNA. The PCR product was ligated into pBluescript and the
                    deleted in Fas dell"
                                                                                             recombinant plasmid was used to transfect E. coli DH5-alpha cells. The
    domain
                    169..314
                                                                                             insert sequence of pBluescript-Fas-delta-TM encoded the protein
FT
                    /label= Cytoplasmic_domain ...
                                                                                        CC given in R76238.
    peptide
                    164...173
                                                                                        SO Sequence 314 AA;
FT
                    /note= "preferred peptide from breakpoint region
                    (claim 4, page 132)
                                                                                                                 6.7%; Score 182; DB 13; Length 314;
    peptide
                    164...174
                                                                                          Best Local Similarity 35.6%; Pred. No. 6.12e-06;
                    /note= "preferred peptide from breakpoint region"
                                                                                          Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;
    peptide
                    /note= "preferred peptide from breakpoint region"
                                                                                                82 cvpcqeqkeytdkahfsskcrrcrlcdeqhqleveinctrtqntkcrckpnffcnstvce 141
PN W09620206-A1.
                                                                                               PD 04-JUL-1996.
PF 22-DEC-1995; U17083.
    23-DEC-1994: US-371263.
                                                                                              142 hcdpc-tkcehgiik--ectltsntkckee 168
    (UABR-) UAB RES FOUND.
                                                                                              154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNE 183
PI Cheng J, Liu C, Mountz JD, Zhou T;
DR WPI: 96-321796/32.
    N-PSDB: T34527.
PT Natural, soluble form of Fas antigen secreted by human cells is
                                                                                        RESULT 13
PT result of alternative mRNA processing - used to diagnose
                                                                                        ID R24083 standard: Protein: 159 AA.
    Fas-associated disease, e.g. systemic lupus erythematosus
                                                                                        AC R24083;
    Claim 4: Page 114-16: 152pp: English.
                                                                                        DT
                                                                                             05-NOV-1992 (first entry)
   A natural, soluble Fas antigen variant (R99682), designated Fas
                                                                                             Truncated TNF-alpha 55kD receptor.
    dell, and other Fas variants (R99683-85) are derived by alternative
                                                                                        KW tumour necrosis factor alpha; extracellular binding domain;
    splicing of Fas gene transcripts. A cDNA clone (T34527) coding for
                                                                                             treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
    the variant was obtd. from human peripheral blood mononuclear cells.
                                                                                        KW
                                                                                             malaria; viral meningits; graft versus host disease;
    The Fas dell variant lacks the transmembrane domain of insoluble
                                                                                        KW
                                                                                             autoimmune disease; rheumatoid arthritis.
    Fas antigen (R99681). Recombinant dell variant, or fragments of
                                                                                             Homo sapiens.
    it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells.
                                                                                        DN
                                                                                             W09207076-A.
    Detection of increased levels of soluble forms of Fas antigen can
                                                                                        Dn
                                                                                             30-APR-1992.
CC be used to diagnose autoimmune diseases, esp. systemic lupus
                                                                                             18-OCT-1991; G01826.
CC erythematosus and angioimmunoblastic lymphadenopathy.
                                                                                        PR 18-OCT-1990: GB-022648.
SQ Sequence 314 AA;
                                                                                        PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
                                                                                             Brennan FM. Feldmann M. Grav PW. Turner MJC:
                        6.7%; Score 182; DB 18; Length 314;
                                                                                             WPT - 92-167156/20
 Best Local Similarity 35.6%; Pred. No. 6.12e-06;
                                                                                             N-PSDB: 024444.
 Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;
                                                                                             New polypeptide capable of binding human TNF alpha - comprises
                                                                                         PΤ
                                                                                             first three cysteine-rich subdomains of TNF alpha receptor for
       82 cvpcqegkeytdkahfsskcrrcrlcdeghqleveinctrtqntkcrckpnffcnstvce 141
                                                                                             treating autoimmune disease, septic shock, HIV etc.
      Example 1; Fig 10; 43pp; English.
                                                                                             This sequence is a truncated TNF-alpha receptor derivative
Qу
                                                                                             as encoded in pdeltaIII. This was produced as described in
Db
     142 hcdpc-tkcehqiik--ect1tsntkckee 168
                                                                                             024444. This derivative lacks the third cysteine rich subdomain.
                                                                                             It could be used to regulate TNF-alpha mediated responses by binding
          at in taise and raina
     154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNE 183
                                                                                             and sequestering human TNF-alpha e.g. in the treatment of pulmonary
                                                                                             diseases, septic shock, HIV infection, malaria, viral meningitis,
                                                                                             graft versus host disease and autoimmune diseases, esp. rheumatoid
RESULT 12
                                                                                             arthritis.
ID R76238 standard; Protein; 314 AA.
                                                                                             See also 024440-51, R24000, R24080-84, R27585, 029236-8
AC R76238:
                                                                                        SQ Sequence 159 AA;
DT 06-NOV-1995 (first entry)
DE Fas-delta-TM.
                                                                                                                6.6%; Score 179; DB 4; Length 159;
KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
                                                                                          Best Local Similarity 41.2%; Pred. No. 1.08e-05;
KW adoptive immunotherapy; transgenic animal.
                                                                                          Matches 28; Conservative 7; Mismatches 30; Indels 3; Gaps 3;
OS Homo sapiens.
```

```
81 crecesg-sftasenhlrhclscskcrkemggveissctvdrdtvctchagfflrenecv 139
         96 CNPCTEGVDYTIASNNLPSCLLCTVC-KS-GOTNKSSCTTTRDTVCOCEKGSPODKNSPE 153
     140 scsnckks 147
           1 4: :
     154 MCRTCRTG 161
RESULT 14
ID R27866 standard; Protein; 326 AA.
    11-MAR-1993 (first entry)
    Myxoma virus T2 protein.
    Polymerase chain reaction; TNF antagonist; tumour necrosis factor.
    W09217583-A.
    15-OCT-1992.
    29-MAR-1991; U02207.
    29-MAR-1991: WO-U22076.
PA (IMMV) IMMUNEX CORP.
    Goodwin RG, Smith CA.
    WPI; 92-366255/44.
    N-PSDB; Q29745.
PT
    Isolated viral proteins are cytokine (e.g. TNF) antagonists - for
    regulating immune response and for treating cachexia septic shock
    and side effects associated with cytokine therapy
    Claim 3; Page 28; 39pp; English.
    The sequence is that of myxoma virus T2 protein which acts as a
    TNF antagonist by binding TNF and preventing it from binding to TNF
    receptors. It can be used for regulating immune responses, treating
    cachexia or septic shock or to treat side effects associated with
     cytokine therapy, e.g. TNF anti-tumour therapy. It may also be used
    as an immunogen, a reagent in assays and as a binding agent for
CC affinity purifications. See also R27865.
SO Sequence 326 AA;
                          6.6%; Score 180; DB 5; Length 326;
 Best Local Similarity 34.4%; Pred. No. 8.91e-06;
Matches 31: Conservative 20: Mismatches 34: Indels 5: Gaps 4;
       61 cspcknet-ftastnhapacvscrqrctqhlsesqscdktrdrvcdcsaqnycllkqqeq 119
      |:||: :|:|:|:|| |::: || ||| ||:: :: |
96 CNPCTEGYDYTIASNNLPSCLLCTV-CKSGQTNKSSCTTTRDTVCQCEKGSFQDKNSPEM 154
     120 cricapktkcpagyg-vsghtrtgdvlctk 148
     || | : | | | | | | : | : | :
155 CRTC--RTGCPRGMVKVSNCTPRSDIKCKN 182
ID R85072 standard; Protein; 326 AA.
AC R85072:
    16-APR-1996 (first entry)
     Myxoma virus T2 protein.
    Myxoma virus; immunosuppressive; cytokine antagonist;
    tumour necrosis factor antagonist; therapeutic; cachexia;
    septic shock.
    Myxoma virus.
    US5464938-A.
    07-NOV-1995.
    18-AUG-1994: 292549.
    19-OCT-1992: US-963330.
    (IMMV ) Immunex Corp.
    Goodwin RG, Smith CA
    WPI: 95-402861/51
    N-PSDB: T02471.
    New soluble viral proteins that bind tumour necrosis factor - for
    treating cachexia, septic shock, side effects of TNP therapy etc.,
    also useful in assays, affinity purificn. and antibody prodn.
    Claim 1; Columns 31-32; 21pp; English.
CC The myxoma virus T2 protein is a soluble viral protein which
CC binds tumour necrosis factor (TNP), thus inhibiting TNF binding
```

C 13 g

CC to its receptor. T2 protein is useful (when administered by

Search completed: Thu May 14 16:50:59 1998

Job time : 49 secs.

injection or infusion from sustained release implants, etc.) for

treating TNF associated toxicity e.g. side effects of using TNF as

CC an antitumour agent or in cases of cachexia and septic shock where



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:49:23 1998; MasPar time 16.85 Seconds 836.713 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-1

Description: (1-386) from US08918874.pep

Perfect Score: 2715

Sequence: 1 MGLWGQSVPTASSARAGRYP......VGSEKLFYEEDEAGSATSCL 386

Scoring table: PAM 150

Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

miscing tirst 45 sminari

Database: pir

1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 46.756: Variance 102.161: scale 0.458

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	191	7.0	335	2	A40036	apoptosis-mediating s	8.42e-13
2	191	7.0	459	2	I48854	gene murine tumour ne	8.42e-13
3	189	7.0	474	2	B38634	tumor necrosis factor	1.70e-12
4	187	6.9	349	2	D36858	gene G4R protein - va	3.43e-12
5	185	6.8	427	1	GOHUN	nerve growth factor r	6.91e-12
6	184	6.8	461	2	JC4302	tumor necrosis factor	9.79e-12
7	182	6.7	314	2	I37383	FAS soluble protein -	1.96e-11
8	180	6.6	326	1	GQV2ML	T2 protein - myxoma v	
9	176	6.5	324	2	JC2395	Fas antigen - rat	1.56e-10
10	177	6.5	327	2	A46484	apoptosis-mediating m	1.11e-10
11	173	6.4	139	5	1TNRR	tumor necrosis factor	4.36e-10
12	173	6.4	140	5	1NCFA	tumor necrosis factor	4.36e-10
13	173	6.4	142	5	1NCFB	tumor necrosis factor	4.36e-10
14	173	6.4	158	5	1EXTB	tumor necrosis factor	4.36e-10
15	173	6.4	160	5	1EXTA	tumor necrosis factor	4.36e-10
16	173	6.4	455	1	GQHUT1	tumor necrosis factor	4.36e-10
17	170	6.3	416	2	JN0006	nerve growth factor r	1.21e-09
18	171	6.3	425	2	A26431	nerve growth factor r	
19	166	6.1	325	2	B43692	T2 protein - rabbit f	
20	159	5.9	461	1	GQRTT1	tumor necrosis factor	
21	158	5.8	461	2	A35356	tumor necrosis factor	
22	156	5.7	454	1	GQMST1	tumor necrosis factor	
23	156	5.7	454	2	157826	tumor necrosis factor	1.31e-07

24	151	5.6	271	2	S12783	OX40 antigen precurso	6.75e-07
25	151	5.6	272	2	I48700	gene ox40 protein - m	6.75e-07
26	144	5.3	256	2	B32393	T-cell antigen 4-1BB	6.43e-06
· 27	144	5.3	435	2	I54182	tumor necrosis factor	6.43e-06
28	137	5.0	255	2	JT0752	lymphocyte activation	5.86e-05
29	134	4.9	260	1	A46517	CD27 antigen precurso	1.49e-04
30	127	4.7	493	2	JC5486	membrane glycoprotein	1.26e-03
31	125	4.6	595	2	A42086	CD30 antigen precurso	2.29e-03
32	118	4.3	250	1	A49053	CD27 antigen precurso	1.80e-02
33	111	4.1	183	2	S52904	virion protein 113L -	1.32e-01
34	111	4.1	185	2	S52903	virion protein j13L -	1.32e-01
35	110	4.1	277	2	A60771	B-cell activation pro	1.74e-01
36	110	4.1	512	2	I80311	sepC protein - Escher	1.74e-01
37	108	4.0	85	2	155492	myosin heavy chain -	3.02e-01
38	109	4.0	176	2	S52914	virion protein j13L -	2.29e-01
39	109	4.0	189	2	S52907	virion protein j13L -	2.29e-01
40	109	4.0	191	2	\$52905	virion protein j13L -	2.29e-01
41	109	4.0	420	2	B38104	LFY floral meristem i	2.29e-01
42	109	4.0	1790	1	MMFFB1	laminin chain B1 prec	2.29e-01
43	108	4.0	3133	2	S52093	hemocytin silkworm	3.02e-01
44	105	3.9	189	2	\$52902	virion protein 113L -	6.84e-01
45	104	3.8	431	1	BWBSSY	preprotein translocas	8.95e-01

ALIGNMENTS

RESULT 1	
ENTRY	A40036 #type complete
*****	apoptosis-mediating surface antigen Fas precursor - humanALTERNATE_N
TITLE	
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	17-Jan-1992 *sequence_revision 17-Jan-1992 *text_change
ACCESSIONS	10-Sep-1997 A40036; S24543; A38142
REFERENCE	A40036
#authors	Itoh, N.: Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima,
	S.I.; Sameshima, M.; Hase, A.; Seto, Y.; Nagata, S.
#journal	Cell (1991) 66:233-243
#title	The polypeptide encoded by the cDNA for human cell surface
	antigen Fas can mediate apoptosis.
	nces MUID:91309137
#accession	A40036
##status	preliminary
	_type mRNA
##residues	
	ferences GB:M67454; NID:g182409; PID:g182410
REFERENCE	\$24543
#authors	Krammer, P.H. submitted to the EMBL Data Library, February 1992
#submission	submitted to the EMBL Data Library, February 1992
#accession	
##status	
	_type mRNA
##residues	
	ferences EMBL:X63717; NID:g28741; PID:g28742
REFERENCE	A38142
#authors	Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.;
	Klas, C.; Li-Weber, M.; Richards, S.; Dhein, J.; Trauth,
	B.C.; Ponsting, H.; Krammer, P.H.
#journal	J. Biol. Chem. (1992) 267:10709-10715
#title	Purification and molecular cloning of the APO-1 cell surface
	antigen, a member of the tumor necrosis factor/nerve growth
	factor receptor superfamily. Sequence identity with the Fas
	antigen. nces MUTD:92268122
	A38142
	The state of the s
##status	
	_type nucleic acid 1-134,'Q',136-335 ##label OEH
	1-134, 'Q',130-333 ##IADEL UEH

sequence extracted from NCBI backbone (NCBIP:103810) in NCBI backbone the source is designated as mouse

##experimental source SKW6.4 cells

GDB:APT1

##note

##note GENETICS

#gene

```
#cross-references MUID:91187885
      ##cross-references GDB:132671: OMIM:134637
   #map position 10g24.1-10g24.1
                                                                                               #accession B38634
                                                                                                 ##molecule_type mRNA
CLASSIFICATION #superfamily NGF receptor repeat homology
                apoptosis; surface antigen; transmembrane protein
                                                                                                              1-474 ##label LEW
                                                                                                  ##residues
                                                                                                 ##cross-references GB:M60469; NID:g199827; PID:g199828
ספוותגסס
   1-16
                     #domain signal sequence #status predicted #label SIG\
                                                                                           REFERENCE
                                                                                                            A40254
                     #domain NGF receptor repeat homology #label NG4\
                                                                                              #authors
                                                                                                            Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
   85-128
                                                                                                            C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
Mol. Cell. Biol. (1991) 11:3020-3026
  174-190
                     #domain transmembrane #status predicted #label TMM
                #length 335 #molecular-weight 37732 #checksum 4899
                                                                                               #iournal
SHMMARY
                                                                                               #title
                                                                                                            Molecular cloning and expression of the type 1 and type 2
                         7.0%; Score 191; DB 2; Length 335;
                                                                                                             murine receptors for tumor necrosis factor.
  Onerv Match
  Best Local Similarity 35.1%; Pred. No. 8.42e-13;
Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;
                                                                                               #cross-references MUID:91246168
                                                                                               #accession A40254
##molecule_type mRNA
                                                                                                                1-474 ##label GOO
       82 CVPCOEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTONTKCRCKPNFFCNSTVCE 141
                                                                                                 ##residues
                                                                                                 ##cross-references GB:M60469; NID:q199827; PID:q199828
      REFERENCE
                                                                                                            S54816
0v
                                                                                                            Kissonerghis, M.: Fellowes, R.: Feldmann, M.; Chernajovsky,
                                                                                               tauthors
      142 HCDPC-TKCRHGTTK--ECTLTSNTKCKREGSRSNLG 175
                                                                                               #submission submitted to the EMBL Data Library, May 1995
          154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTG 190
                                                                                               *description Characterization of the promoter region of the murine p75-TNF
                                                                                                              receptor.
                                                                                                           S54816
                                                                                               #accession
RESULT 2
                                                                                                 ##status
                                                                                                                 preliminary
                                                                                                 ##molecule_type DNA
ENTRY
                I48854
                           #type fragment
                                                                                                              1-22 ##label KIS
                gene murine tumour necrosis factor receptor 2 protein - mouse
                                                                                                  ##cross-references EMBL: X87128; NID: q809043; PID: q809044
TIPIP
ORGANISM
                 #formal_name Mus musculus #common_name house mouse
                                                                                            CLASSIFICATION *superfamily tumor necrosis factor receptor type 2; NGF
                02-Jul-1996 *sequence_revision 02-Jul-1996 *text_change
                                                                                                              receptor repeat homology
שתגם
                                                                                                            cytokine receptor; transmembrane protein
                  23-Feb-1997
                                                                                            KEYWORDS
ACCESSIONS
                T48854
                                                                                           FEATURE
                                                                                                                 #domain signal sequence #status predicted #label SIG\
REFERENCE
                T48854
                                                                                               1-22
   #authors
                Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
                                                                                               23-474
                                                                                                                 *product tumor necrosis factor receptor type 2 *status
                                                                                                                  predicted #label MAT\
                Mamm. Genome (1994) 5:726-727
   #iournal
                                                                                                                 #domain NGF receptor repeat homology #label NG1\
   #title
                Allelic variation of the type 2 tumor necrosis factor
                                                                                                                 #domain NGF receptor repeat homology #label NG2\
                                                                                               79-120
                  receptor gene.
   #cross-references MUID:95178848
                                                                                               166-203
                                                                                                                 #domain NGF receptor repeat homology #label NG4
                                                                                                            #length 474 #molecular-weight 50319 #checksum 7767
                                                                                            STIMMARY
   taccession
                T48854
                    preliminary; translated from GB/EMBL/DDBJ
      ##status
                                                                                                                     7.0%; Score 189; DB 2; Length 474;
      ##molecule_type mRNA
                                                                                              Best Local Similarity 27.6%; Pred. No. 1.70e-12;
      ##residues 1-459 ##label RES
                                                                                              Matches 29: Conservative 27: Mismatches 44: Indels 5; Gaps 5;
      ##cross-references EMBL:X76401; NID:g433830; PID:g433831
CLASSIFICATION #superfamily tumor necrosis factor receptor type 2; NGF
                  receptor repeat homology
                                                                                                   76 CADCEASM-YTOVWNOFRTCLSCSSSCTTDQVEIRACTKQQNRVCACEAGRYCALKTHSG 134
                                                                                                      VARMMIN
                #length 459 #checksum 3156
                                                                                                   96 CNPCTEGVDYTIASNNLPSCLLCTV-CKSGOTNKSSCTTTRDTVCQCEKGSFQD-KNSPE 153
                         7.0%; Score 191; DB 2; Length 459;
  Best Local Similarity 27.6%; Pred. No. 8.42e-13;
                                                                                                  135 SCROCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTD 179
                                                                                                  || || :| || ::::| ::::: || ::::: || ::::: || 154 MCRTC-RTG-CPRGMYKVSNCTPRSDIKCKNESAASSTGKTPAAE 196
  Matches 29: Conservative 27: Mismatches 44: Indels 5: Gaps 5:
       61 CADCEASM-YTOVWNOFRTCLSCSSSCSTDOVETRACTKOONRVCACEAGRYCALKTHSG 119
         96 CNPCTEGVDYTIASNNLPSCLLCTV-CKSGOTNKSSCTTTRDTVCOCEKGSFOD-KNSPE 153
                                                                                            RESULT 4
                                                                                           ENTRY
                                                                                                            D36858
                                                                                                                      #type complete
      120 SCROCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTD 164
                                                                                                            qene G4R protein - variola virusALTERNATE_NAMES B28R protein (COP)
          HELLS I I ISSUED IN SECTION
                                                                                            TITLE
      154 MCRTC-RTG-CPRGMVKVSNCTPRSDIKCKNRSAASSTGKTPAAE 196
                                                                                                             #formal name variola virus
                                                                                            ORGANISM
                                                                                                            30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                           DATE
                                                                                                              10-Sep-1997
                                                                                            ACCESSIONS
                                                                                                            D36858; S46888; S32385; S35987
RESULT 3
                                                                                                            A36859
ENTRY
                B38634
                           #type complete
                                                                                            REFERENCE
                                                                                               #authors
                                                                                                            Blinov, V.M.
                 tumor necrosis factor receptor type 2 precursor - mouseORGANISM
                                                                                               #submission submitted to GenBank, November 1992
TITLE
                 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                                                                                               #description not shown.
DATE
                                                                                               #accession D36858
                  08-San-1997
                                                                                                                 preliminary
ACCESSIONS
                 B38634; A40254; S54816
                                                                                                  ##status
REFERENCE
                                                                                                  ##molecule_type DNA
                Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
                                                                                                  ##residues
                                                                                                                 1-349 ##label BLI
   #authors
                                                                                                  ##cross-references GB:X69198; NID:q456758; PID:q457087
   #journal
                 Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
                                                                                                 ##experimental_source strain India-1967, ssp. major, isolate Ind3
                Cloning and expression of cDNAs for two distinct murine tumor
                                                                                            REFERENCE
   #fitle
                                                                                                            Kolykhalov, A.A.: Blinov, V.M.; Gytorov, V.V.; Pozdnyakov,
                                                                                               #authors
                  necrosis factor receptors demonstrate one receptor is
                  species specific.
                                                                                                              S.G.: Chizhikov, V.E.: Frolov, I.V.: Totmenin, A.V.;
```

nh

Qy

Db

##note

this sequence has been corrected by a note added in

```
Shchelkunov, S.N.: Sandakhchiev, L.S.
                                                                                                                  proof to follow the nucleotide translation from a
   #submission submitted to the EMBL Data Library, April 1992
                                                                                                                  published report
                                                                                                            S21689
   #description Mucleotide sequence analysis of the region of variola virus
                                                                                           REFERENCE
                  XhoI F O H P O genome fragment.
                                                                                              tauthors
                                                                                                            Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
   #accession
                S46888
                                                                                                            Arch. Biochem. Biophys. (1992) 294:244-252
                                                                                              #iournal
                    preliminarv
      ##status
                                                                                                            Structural domains of the extracellular domain of human nerve
                                                                                              #title
      ##molecule_type DNA
                                                                                                              growth factor receptor detected by partial proteolysis.
      ##residues
                     1-349 ##label KOL
                                                                                              #cross-references MUID:92198017
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                                                                                              #accession S21689
     ##experimental_source strain India-1967, isolate Ind3
                                                                                                                preliminary
                                                                                                 ##status
REFERENCE
                S32385
                                                                                                 ##molecule_type protein
                Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
   #authors
                                                                                                ##residues
                                                                                                                183-208 ##label VIS
   #iournal
                FEBS Lett. (1993) 319:80-83
                                                                                           REFERENCE
   #title
                Genes of variola and vaccinia viruses necessary to overcome
                                                                                                            Sehgal, A.; Patil, N.; Chao, M.
                                                                                              #authors
                  the host protective mechanisms.
                                                                                              #iournal
                                                                                                            Mol. Cell. Biol. (1988) 8:3160-3167
                $32385
   #accession
                                                                                              #title
                                                                                                            A constitutive promoter directs expression of the nerve
      ##molecule_type DNA
                                                                                                             growth factor receptor gene.
                     31-168 ##label SHC
      iireci duec
                                                                                              #cross-references MUID:89096903
      ##cross-references EMBL:X69198
                                                                                              #accession
     ##experimental_source strain India-1967, ssp. major
                                                                                                                preliminary; translated from GB/EMBL/DDBJ
                                                                                                 ##etatue
GENETICS
                                                                                                 ##molecule_type DNA
   #gene
                                                                                                                1-22 ##label RES
                                                                                                 ##residues
CLASSIFICATION #superfamily NGF receptor repeat homology
                                                                                                 ##cross-references GB:M21621: NID:q189206: PID:q189207
FEATURE
                                                                                           COMMENT This receptor is found on sensory and sympathetic neurons; on
   68-109
                     #domain NGF receptor repeat homology #label NG2\
                                                                                                        neuroblastoma cells, and on a variety of nonneuronal derivatives
   110-151
                     #domain NGF receptor repeat homology #label NG3
                                                                                                        of the neural crest.
CUMMARY
                #length 349 #molecular-weight 38189 #checksum 2016
                                                                                           COMMENT The cysteine-rich region of the extracellular domain may form part
                                                                                                        or all of the NGF-binding site.
                        6.9%; Score 187; DB 2; Length 349;
                                                                                           COMMENT
                                                                                                      This protein is thought to form a high-affinity receptor when it
 Best Local Similarity 37.1%; Pred. No. 3.43e-12;
                                                                                                        associates with the 140K trk proto-oncogene, which contains an
 Matches 33; Conservative 18; Mismatches 31; Indels 7; Gaps 6;
                                                                                                        intracellular tyrosine kinase domain.
                                                                                           COMMENT
                                                                                                      This receptor undergoes both N- and O-linked glycosylation.
       65 CTPCGSGT-FTSRNNHLPACLSCNGRCNSNOVETRSCNTTHNRICECSPGYYCLLKGSSG 123
                                                                                           GENETICS
      ‡gene
                                                                                                 ##cross-references GDB:120234: OMIM:162010
                                                                                               #map_position 17q21-17q22
     124 -CKACVSOTKCGIGYG-VSGHTSVGDVIC 150
                                                                                           CLASSIFICATION #superfamily nerve growth factor receptor; NGF receptor
          1::1 :1 1 1 11 1: :1: 1
                                                                                                              repeat homology
     154 MCRTC -- RTGCPRGMVKVSNCTPRSDIKC 180
                                                                                           KEYWORDS
                                                                                                            duplication; glycoprotein; heterodimer; monomer;
                                                                                                             phosphoprotein; receptor; transmembrane protein
                                                                                           FEATURE
PECHIT 5
                                                                                              1-28
                                                                                                                 #domain signal sequence #status predicted #label SIG\
ENTRY
                           #type complete
                                                                                              29-427
                                                                                                                 *product nerve growth factor receptor #status
                                                                                                                  experimental #label MAT\
TITLE
                nerve growth factor receptor precursor, low affinity - humanALTERNATE_N
                                                                                              29-250
                                                                                                                 #domain extracellular #status predicted #label EXT\
ODCANTON
                #formal_name Homo sapiens #common_name man
                                                                                              29-190
                                                                                                                 #region cysteine-rich\
DATE
                31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
                                                                                                                 #domain NGF receptor repeat homology #label NG1\
                                                                                              32-65
                  20-Mar-1998
                                                                                              67-108
                                                                                                                 #domain NGF receptor repeat homology #label NG2\
ACCESS IONS
                A25218: A60204: S21689: T57638
                                                                                              109-147
                                                                                                                 #domain NGF receptor repeat homology #label NG3\
REFERENCE
                                                                                                                 #domain NGF receptor repeat homology #label NG4\
                A25218
                                                                                              149-189
  #authors
                Johnson, D.: Lanahan, A.: Buck, C.R.: Sehgal, A.: Morgan, C.:
                                                                                              197-248
                                                                                                                 #region serine/threonine-rich\
                                                                                                                 #domain transmembrane #status predicted #label TRM\
                  Mercer, E.; Bothwell, M.; Chao, M.
                                                                                              251-272
   #journal
                Cell (1986) 47:545-554
                                                                                              273-427
                                                                                                                 #domain intracellular #status predicted #label INT\
   #fitle
                Expression and structure of the human NGF receptor.
                                                                                                                 #binding_site_carbohydrate (Asn) (covalent) #status
                                                                                              60
                                                                                                                  predicted
   #cross-references MUID:87051725
                                                                                                            #length 427 #molecular-weight 45183 #checksum 7426
   taccossion
                A25218
                                                                                           SUMMARY
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      ##residues
                    1-427 ##label JOH
                                                                                             Query Match
                                                                                                                    6.8%; Score 185; DB 1; Length 427;
     ##cross-references GB:M14764: NID:g189204: PID:g189205
                                                                                             Best Local Similarity 29.4%; Pred. No. 6.91e-12;
                                                                                             Matches 25: Conservative 21: Mismatches 37: Indels 2: Gaps 2:
PERFERENCE
   #authors
                Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman,
                  G.; Thompson, S.; Grob, P.; Ross, A.H.; Bothwell, M.;
                                                                                                  64 CEPCLDSVTFSDVVSATEPCKPCTECVGLOSMSAPCVEADDAVCRCAYGYYQD-ETTGRC 122
                  Atkinson, B.F.; Koprowski, H.
                                                                                                     #journal
                J. Neurochem. (1987) 48:225-232
                                                                                                  96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGOTNKSSCTTTRDTVCOCEKGSFODKNSPEMC 155
   #fitle
                Purification and amino terminal sequencing of human melanoma
                 nerve growth factor receptor.
                                                                                                 123 EACRY-CEAGSGLVFSCODKONTVC 146
   #cross-references MUID: 87085574
                                                                                                 :|| | | | :| : : |
156 RTCRTGCPRGMVKVSNCTPRSDIKC 180
   taccession
                A60204
     ##molecule_type protein
                     29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 ##labe1
     ##residues
                                                                                            RESULT 6
                                                                                                                      #type complete
      ##experimental_source melanoma cell line A875
                                                                                           PNTRY.
                                                                                                            JC4302
```

```
tumor necrosis factor receptor p55 - pigORGANISM
TITLE
                                                                       #formal name S
                29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                                                                                                  82 CVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTONTKCRCKPNFFCNSTVCE 141
DATE
                                                                                           Db
                                                                                                  12-Dec-1997
ACCESSIONS
                JC4302: PC4093
                                                                                           Q٧
REFERENCE
                JC4302
                                                                                                 142 HCDPC-TKCEHGIIK--RCTLTSNTKCKEE 168
   #authors
                Suter, B.; Pauli, U.
                                                                                           nh
                Gene (1995) 163:263-266
                                                                                                     TELL FIELD BY BUILDING
   #iournal
                Cloning of the cDNA encoding the porcine p55 tumor necrosis
                                                                                                 154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNE 183
   #title
                  factor receptor.
   #accession
                JC4302
     ##molecule_type mRNA
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                    1-461 ##label SUT
                                                                                           ENTRY
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                                                                                           TITLE
                                                                                                           T2 protein - myxoma virus (strain Lausanne)ORGANISM
                                                                                                                                                                      #formal
                                                                                                           31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
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                                                                                                             24-Oct-1997
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                                                                                                           A40566
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                                                                                           REFERENCE
                                                                                                           A40566
GENERICS
                                                                                                           Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
                                                                                              #authors
   #gene
                                                                                                            Virology (1991) 184:370-382
CLASSIFICATION
                #superfamily tumor necrosis factor receptor type 1; NGF
                                                                                              #iournal
                                                                                                           Myxoma virus expresses a secreted protein with homology to
                  receptor repeat homology
                                                                                              #fifle
                glycoprotein; kidney; receptor; transmembrane protein; tumor
                                                                                                             the tumor necrosis factor receptor gene family that
KEYWORDS
                                                                                                             contributes to viral virulence.
FEATURE
   1-29
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                                                                                              #accession A40566
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                                                                                                 ##molecule type DNA
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   44-82
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   211-231
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                                                                                                             homology
   361-447
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                                                                                           KEYWORDS
                                                                                                           qlycoprotein
                                                                                           FEATURE
                                                                                              64-105
   54,145,151
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                                                                                                                #domain NGF receptor repeat homology #label NG2\
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                                                                                                                #domain NGF receptor repeat homology #label NG3\
                       predicted
                                                                                                                #binding site carbohydrate (Asn) (covalent) #status
SUMMARY
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                                                                                           STIMMARY
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  Best Local Similarity 36.3%; Pred. No. 9.79e-12;
                                                                                                                    6.6%; Score 180; DB 1; Length 326;
  Matches 33; Conservative 17; Mismatches 32; Indels 9; Gaps 7;
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                                                                                             Best Local Similarity 34.4%; Pred. No. 3.93e-11;
                                                                                                      31; Conservative 20; Mismatches 34; Indels 5; Gaps 4;
       81 CRECDNGT-FTASENHLTOCLSCSKCRSEMSOVEISPCTVDRDTVCGCRKNOYR-KYWSE 138
          61 CSPCKNET-FTASTNHAPACVSCRGRCTGHLSESOSCDKTRDRVCDCSAGNYCLLKGOEG 119
       96 CNPCTEGVDYTIASNNLPSCLLCTVCKS--GOTNKSSCTTTRDTVCOCEKGSFODKNSPE 153
                                                                                                  |:||: :|:||:|| | : :: || ||| ||: :: |
96 CNPCTECUDYTIASNNLPSCLICTY-CKSGOTNKSSCTTTRDTYCOCEKGSFODKNSPEM 154
      139 TLFOCLNCSL-CPNGTVQLP-CLEKQDTICN 167
          3 T. L. H. H. L. C. L. C. L. C.
                                                                                                 120 CRICAPKTKCPAGYG-VSGHTRTGDVLCTK 148
      154 -M--CRTCRTGCPRGMVKVSNCTPRSDIKCK 181
                                                                                                     11 1 11 11 11 11 11 11 11 11
                                                                                                 155 CRTC -- RTGCPRGMVKVSNCTPRSDIKCKN 182
premir 7
ENTRY
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                                                                                           RESULT 9
                                                                                                           JC2395
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                                                                                                                      #type complete
TITLE
                                                           #formal name Homo sapiens
                                                                                           ENTRY
                 02-Jul-1996 #sequence revision 02-Jul-1996 #text change
በልጥድ
                                                                                                           Fas antigen - ratORGANISM
                                                                                                                                             #formal_name Rattus norvegicus #co
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                  02-Jul-1996
                                                                                                           20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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                                                                                                             10-Sep-1997
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                                                                                                            JC2395; PC2246
   #authors
                 Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
                                                                                           ACCESSIONS
                J. Immunol. (1995) 154:2706-2713
                                                                                           REFERENCE
                                                                                                           JC2395
   #iournal
                                                                                                           Kimura, K.; Wakatsuki, T.; Yamamoto, M.
                 Three functional soluble forms of the human
                                                                                              #authors
   #title
                                                                                                            Biochem, Biophys, Res. Commun, (1994) 198:666-674
                  apoptosis-inducing Fas molecule are produced by alternative
                                                                                              #iournal
                                                                                                           A variant mRNA species encoding a truncated from of Fas
                  splicing
                                                                                              #title
                                                                                                             antigen in the rat liver.
   #cross-references MUID: 95181785
                                                                                              #accession
                                                                                                           102395
   #accession I37383
                     preliminary; translated from GB/EMBL/DDBJ
      Ekotatno
                                                                                                 ##molecule type mRNA
                                                                                                                1-324 ##label KIM
      ##molecule type mRNA
                                                                                                 ttresidues.
                                                                                                 ##cross-references DDBJ:D26112; NID:g468486; PID:d1005650; PID:g468487
                    1-314 ##label RES
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                                                                                                 ##experimental source thymus
      ##cross-references EMBL: 247993; NID: q728578; PID: q695539
                #length 314 #molecular-weight 35386 #checksum 655
                                                                                              #accession PC2246
VAGMMIN
                                                                                                 ##molecule_type mRNA
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                                                                                                 ##cross-references DDBJ:D26113: NID:q468488: PID:d1005651; PID:q468489
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```

```
GENETICS
                                                                                           ٥v
                                                                                                 93 TGACNPCTEGVDYTIASNNLPSCLLCTVCKSGOT-N-KSSCTTTRDTVCQCEKGSFQDKN 150
  #introns
                62/1
CLASSIFICATION #superfamily NGF receptor repeat homology
                                                                                           Πh
                                                                                                 135 GCEHCVRC-ASCEHGTLE-P-CTATSNTNCRKQSP 166
KEYWORDS
                transmembrane protein
                                                                                                    a li li telel a a a lla la dedic
FEATURE
                                                                                                 151 SPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESA 185
                                                                                           Qy
  1-21
                     #domain signal sequence #status predicted #label SIG\
  22-324
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  81-124
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                                                                                              #authors
                                                                                                           Banner, D.W.
       77 TCHPCTEGEEYTDRKHYSDKCRRCAFCDEGHGLEVETNCTRTONTKCRCKENFYCNASLC 136
                                                                                              #submission submitted to the Brookhaven Protein Data Bank, May 1994
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                                                                                                           Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                                                                                              #authors
     137 DHCYHC-TSCGLEDI-LEPCTRTSNTKCKKOSS 167
                                                                                                             H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
                                                                                                           Cell (1993) 73:431-445
     : | | |:| :: || |: ||::|:
153 EMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESA 185
                                                                                              #iournal
                                                                                                           Crystal structure of the soluble human 55 kd TNP
                                                                                              #title
                                                                                                             receptor-human TNFbeta complex; implications for TNF
                                                                                                             receptor activation.
RESULT 10
                                                                                           REFERENCE
                                                                                                           TN034093
                A46484
                                                                                                           D'arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;
ENTRY
                          #type complete
                                                                                              #authors
                                                                                                             Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;
TITLE
                apoptosis-mediating membrane-associated polypeptide Fas -
                                                                                                             Lesslauer, W.
ORGANISM
                #formal_name Mus musculus #common name house mouse
                                                                                              #journal
                                                                                                           J. Mol. Biol. (1993) 229:555
DATE
                18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                              #title
                                                                                                           Crystallization and preliminary analysis of tnf-beta and a
                  20-Mar-1998
                                                                                                             tnf-beta-55 kd tnf receptor complex.
ACCESSIONS
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                                                                                           COMMENT
                                                                                                     Resolution: 2.85 angstroms
REFERENCE
                A46484
                                                                                           COMMENT
                                                                                                     Determination: X-ray diffraction
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                Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.;
                                                                                           KEYWORDS
                  Copeland, N.G.; Jenkins, N.A.; Nagata, S.
                                                                                           PEATURE
  #iournal
                J. Immunol. (1992) 148:1274-1279
                                                                                                                #disulfide bonds\
                                                                                              1-15
  ####1e
                The cDNA structure, expression, and chromosomal assignment of
                                                                                                                #disulfide_bonds\
                                                                                              16-29
                  the mouse Fas antigen.
                                                                                              19-38
                                                                                                                #disulfide_bonds\
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                                                                                              41-56
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                                                                                              62-82
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                                                                                              84-100
                                                                                                                #disulfide_bonds\
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                                                                                                                #disulfide_bonds\
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                                                                                           SUMMARY
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                                                                                             Onery Match
                                                                                             Best Local Similarity 37.1%; Pred. No. 4.36e-10;
                Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
   fauthore
                Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760
                                                                                             Matches 33: Conservative 12: Mismatches 37: Indels 7: Gaps 6:
   #iournal
   #fifle
                Aberrant transcription caused by the insertion of an early
                  transposable element in an intron of the Fas antigen gene
                                                                                                  38 CRECESG-SFTASENHLRHCLSCSKCRKEMGOVEISSCTVDRDTVCGCRKNOYRHYWSEN 96
                                                                                                     of lpr mice.
                                                                                                  96 CNPCTEGVDYTIASNNLPSCLLCTVC-KS-GQTNKSSCTTTRDTVCQCEKGSPODKNSPE 153
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                                                                                           0ν
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                                                                                                  97 LFOCFNCSL-CLNGTVHLS-CQEKONTVC 123
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                                                                                                : | | | | | | : | | : : |
154 M--CRTCRTGCPRGMVKVSNCTPRSDIKC 180
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     ##note
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CLASSIFICATION #superfamily NGF receptor repeat homology
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                                                                                                           1NCFA
KRYWORDS
                transmembrane protein
                                                                                                           tumor necrosis factor receptor 55 kd extracellular domain
FEATURE
                                                                                           TITLE
                                                                                                             contains residues 12 172 of the mature receptor sequence,
  81-124
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CUMMADA
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 Query Match
                                                                                                           #formal_name Homo sapiens #common_name man
                        6.5%; Score 177; DB 2; Length 327;
                                                                                           ODCANTON
                                                                                                           expressed in Escherichia coli, residue 11 is mutated to met
  Best Local Similarity 30.5%: Pred. No. 1.11e-10:
                                                                                              #note
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                                                                                                           A66195
      75 TPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTONTKCKCKPDFYCDSP 134
                                                                                              #authors
                                                                                                           Naismith, J.H.; Sprang, S.R.
                                                                                              #submission submitted to the Brookhaven Protein Data Bank, October 1994
         Talumed as a filled a completely of
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COMMENT

Determination: X-ray diffraction

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COMMENT
                                                                                                       R-value: no refinement
   #cross-references PDB:1NCF
REFERENCE
                TN029039
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                Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
                                                                                             FEATURE
  #authors
                  K.; Naismith, J.H.; Sprang, S.R.
                                                                                                2-16
                                                                                                                  #disulfide_bonds\
                                                                                                17-30
                                                                                                                  #disulfide bonds\
   #iournal
                J. Mol. Biol. (1994) 239:332
   #title
                Two crystal forms of the extracellular domain of type i tumor
                                                                                                20-39
                                                                                                                  #disulfide bonds\
                                                                                               42-57
                                                                                                                  #disulfide bonds\
                   necrosis factor receptor.
REFERENCE
                A40737
                                                                                                60-75
                                                                                                                  #disulfide bonds\
                                                                                                63-83
                                                                                                                  #disulfide bonds\
   Hauthors
                Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                  H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
                                                                                                85-101
                                                                                                                  #disulfide bonds\
   #iournal
                Cell (1993) 73:431-445
                                                                                                104-116
                                                                                                                  #disulfide bonds\
                Crystal structure of the soluble human 55 kd TNF
                                                                                                                  #disulfide bonds\
  #title
                                                                                                107-124
                   receptor-human TNFbeta complex: implications for TNF
                                                                                                126-137
                                                                                                                  #disulfide_bonds
                                                                                                             #length 142 #molecular-weight 16046 #checksum 1225
                   receptor activation.
                                                                                             CITMMADY
COMMENT
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                                                                                                                      6.4%; Score 173; DB 5; Length 142;
COMMENT
          Determination: X-ray diffraction
                                                                                               Onery Match
                                                                                               Best Local Similarity 37.1%; Pred. No. 4.36e-10;
COMMENT
          R-value: no refinement
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KEYWORDS
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FRATURE
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   5-19
   20-33
                      *disulfide bonds\
                                                                                                       E T T 31 : 131 TE 13 TE 1 TE 1 THE THIRD THE 31 TE
                                                                                                    96 CMPCTEGVDYTTASHNI,PSCLICTVC-KS-GOTNKSSCTTTRDTVCOCEKGSFODKNSPE 153
   23-42
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   45-60
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   63-78
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   66-86
                      #disulfide bonds\
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   107-119
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                                                                                                              1EXTR
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                                                                                             TITLE
                                                                                                              tumor necrosis factor receptor extracellular domain, chain B
                                                                                                             extracellular domain of the 55kda tumor necrosis factor
                                                                                             PDB_TITLE
                                                                                                               receptor, crystallized at ph3.7 in p 21 21 21.
  Matches 33; Conservative 12; Mismatches 37; Indels 7; Gaps 6;
                                                                                             ORGANISM
                                                                                                              #formal name Homo sapiens #common name man
                                                                                                             expressed in Escherichia coli, the construct contains
       42 CRECESG-SFTASENHLRHCLSCSKCRKEMGOVEISSCTVDRDTVCGCRKNOYRHYWSEN 100
                                                                                                #note
                                                                                                               residues 12 to 172 of the mature sequence of the entire
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                                                                                                               expression system
                                                                                             DECEDENCE
      101 LFQCFNCSL-CLNGTVHLS-CQEKQNTVC 127
                                                                                                             A65560
                                                                                                              Naismith, J.H.; Sprang, S.R.
         #authors
                                                                                                             submitted to the Brookhaven Protein Data Bank, July 1996
      154 M -- CRTCRTGCPRGMVKVSNCTPRSDIKC 180
                                                                                                #enhmission
                                                                                                #cross-references PDB:1EXT
                                                                                             PERFERENCE
RESULT 13
                                                                                                #authors
                                                                                                              Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
                                                                                                              J. Biol. Chem. (1995) 270:13303
ENTRY
                INCER
                           #type complete
                                                                                                #iournal
                                                                                                             Crystallographic evidence for dimerization of unliganded
                                                                                                #title
TITLE
                tumor necrosis factor receptor 55 kd extracellular domain
                                                                                                               tumor necrosis factor receptor.
                                                                                             DECEDENCE
                                                                                                              TM026252
                  contains residues 12 172 of the mature receptor sequence,
                                                                                                             Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
                   chain B - hu
                                                                                                #authors
ALTERNATE_NAMES stnfrl; type i receptor
                                                                                                               K.; Naismith, J.H.; Sprang, S.R.
                                                                                                              J. Mol. Biol. (1994) 239:332
ORGANISM
                #formal name Homo sapiens #common name man
                                                                                                #journal
   #note
                expressed in Escherichia coli, residue 11 is mutated to met
                                                                                                #title
                                                                                                              Two crystal forms of the extracellular domain of type i tumor
                                                                                                               necrosis factor receptor.
                  as a result of the expression system
REFERENCE
                                                                                             REFERENCE
                                                                                                             Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
   #authors
                Naismith, J.H.; Sprang, S.R.
                                                                                                #authors
                submitted to the Brookhaven Protein Data Bank, October 1994
                                                                                                               H.J.: Broger, C.: Loetscher, H.: Lesslauer, W.
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                                                                                                             Cell (1993) 73:431-445
   #cross-references PDB: INCP
                                                                                                #iournal
REFERENCE
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                                                                                                              Crystal structure of the soluble human 55 kd TNF
                                                                                                               receptor-human TNFbeta complex: implications for TNF
                Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
   #authors
                   K.; Naismith, J.H.; Sprang, S.R.
                                                                                                               receptor activation.
                                                                                             COMMENT
                                                                                                       Resolution: 1.85 angstroms
   #iournal
                 J. Mol. Biol. (1994) 239:332
   #title
                Two crystal forms of the extracellular domain of type i tumor
                                                                                             COMMENT
                                                                                                       Determination: X-ray diffraction
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                                                                                                       R-value: no refinement
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                                                                                             KEYWORDS
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REFERENCE
                                                                                             FRATURE
   #authors
                 Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                   H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
                                                                                                68-70
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                Cell (1993) 73:431-445
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                                                                                                143-145
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                Crystal structure of the soluble human 55 kd TNF
                                                                                                9-11,19-21
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                   receptor-human TNFbeta complex: implications for TNF
                                                                                                133-136, 139-142
                                                                                                27-31,41-44
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                                                                                                73-76.85-87
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COMMENT
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92-98,101-106

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90-96,99-104

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   20-33
                     #disulfide bonds\
   23-42
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   63-78
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   66-86
                     #disulfide bonds\
   88-104
                     #disulfide bonds\
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   107-119
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      Dh
     101 LFQCFNCSL-CLNGTVHLS-CQEKQNTVC 127
     : | | | | | : | : : |
154 M--CRTCRTGCPRGMVKVSNCTPRSDTKC 180
RESULT 15
                1 EXTA
ENTRY
                           #type complete
TITLE
                tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE
                extracellular domain of the 55kda tumor necrosis factor
                  receptor. crystallized at ph3.7 in p 21 21 21.
ORGANISM
                #formal name Homo sapiens #common name man
   #note
                expressed in Escherichia coli, the construct contains
                  residues 12 to 172 of the mature sequence of the entire
                  receptor, residue 11 is mutated to met as a result of the
                  expression system
REFERENCE
                A65560
                Naismith, J.H.; Sprang, S.R.
   #authors
   *submission submitted to the Brookhaven Protein Data Bank, July 1996
   #cross-references PDB:1EXT
REFERENCE
   #authors
                Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
   #journal
                J. Biol. Chem. (1995) 270:13303
   #title
                Crystallographic evidence for dimerization of unliganded
                  tumor necrosis factor receptor.
DEPENDENCE
                TN026249
   #authors
                Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
                  K.; Naismith, J.H.; Sprang, S.R.
   #journal
                J. Mol. Biol. (1994) 239:332
   #title
                Two crystal forms of the extracellular domain of type i tumor
                  necrosis factor receptor.
PERFERENCE
                A40737
   #authors
                Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
                  H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
   #iournal
                Cell (1993) 73:431-445
                Crystal structure of the soluble human 55 kd TNF
   #title
                  receptor-human TNFbeta complex; implications for TNF
                  receptor activation.
COMMENT
         Resolution: 1.85 angstroms
COMMENT
          Determination: X-ray diffraction
COMMENT
          R-value: no refinement
KEYWORDS
                binding protein; cytokine; signalling protein
FEATURE
   66-68
                     #region helix (right hand 3-10)\
   141-143
                     #region helix (right hand 3-10)\
   151-154
                     #region helix (right hand alpha)\
   7-9,17-19
                     #region beta sheet\
   131-134,137-140
                     #region beta sheet\
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25-29,39-42

71-74,83-85

#region beta sheet\

#region beta sheet\

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111-115,124-127 #region beta sheet\
   3-17
                     #disulfide bonds\
                     #disulfide bonds\
  18-31
   21-40
                     #disulfide bonds\
   43-58
                     #disulfide bonds\
  61-76
                     #disulfide bonds\
   64-84
                     #disulfide bonds\
   86-102
                     #disulfide_bonds\
   105-117
                     #disulfide_bonds\
   108-125
                     #disulfide_bonds\
   127-138
                     #disulfide bonds\
                     #disulfide_bonds\
  141-154
  144-150
                     #disulfide bonds
                #length 160 #molecular-weight 18065 #checksum 2297
CITMMA DV
                        6.4%; Score 173; DB 5; Length 160;
 Ouerv Match
 Best Local Similarity 37.1%; Pred. No. 4.36e-10;
Matches 33; Conservative 12; Mismatches 37; Indels 7; Gaps 6;
      40 CRECESG-SFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSEN 98
      99 LFOCFNCSL-CLNGTVHLS-COEKONTVC 125
     : | | | | | : | | : : |
154 M--CRTCRTGCPRGMVKVSNCTPRSDIKC 180
Search completed: Thu May 14 16:49:54 1998
Job time : 31 secs.
```

#region beta sheet\

RESULT 1 ID FASA BOVIN



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:47:33 1998; MasPar time 11.24 Seconds

861.719 Million cell updates/sec Tabular output not generated.

Title: >US-08-918-874-1

Description: (1-386) from US08918874.pep 2715

Perfect Score:

Sequence: 1 MGLWGQSVPTASSARAGRYP......VGSEKLFYEEDEAGSATSCL 386

Scoring table: PAM 150

Gap 11

Searched: 69112 segs, 25083644 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot35

1:swissl

Statistics: Mean 48,960; Variance 85,763; scale 0,571

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	216	8.0	323	1	FASA BOVIN	FASL RECEPTOR PRECURSO	6.03e-21
2	191	7.0	335	1		FASL RECEPTOR PRECURSO	
3	189	7.0	474	1	TNR2_MOUSE	TUMOR NECROSIS FACTOR	8.49e-16
4	187	6.9	349	1	VC22_VARV	PROTEIN C22/B28 HOMOLO	2.00e-15
5	185	6.8	427	1			4.71e-15
6	184	6.8				TUMOR NECROSIS FACTOR	7.22e-15
i	180	6.6	326				3.95e-14
8	177	6.5	327		FASA_MOUSE		
9	173	6.4				TUMOR NECROSIS FACTOR	7.47e-13
10	170	6.3	416	1			2.60e-12
11	171	6.3		1	NGFR RAT	LOW-AFFINITY NERVE GRO	1.72e-12
12	166	6.1	325	1	VT2_SFVKA	TUMOR NECROSIS FACTOR	1.36e-11
13	159	5.9				TUMOR NECROSIS FACTOR	2.35e-10
14	158	5.8	461	1	TNR2_HUMAN	TUMOR NECROSIS FACTOR	3.51e-10
15	156	5.7	454			TUMOR NECROSIS FACTOR	7.85e-10
16	151	5.6	271	1	OX40_RAT	OX40L RECEPTOR PRECURS	5.75e-09
17	151	5.6	272	1		OX40L RECEPTOR PRECURS	5.75e-09
18	144	5.3	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	8.88e-08
19	144	5.3	435	1	TNRC HUMAN	LYMPHOTOXIN-BETA RECEP	8.88e-08
20	132	4.9	255	1	41BB_HUMAN	4-1BB LIGAND RECEPTOR	8.39e-06
21	131	4.8	260	1	CD27_HUMAN	CD27L RECEPTOR PRECURS	1.21e-05
22	130	4.8	277	1	OX40_HUMAN	OX40L RECEPTOR PRECURS	1.76e-05
23	125	4.6	595	1	CD30_HUMAN	CD30L RECEPTOR PRECURS	1.08e-04

24	125	4.6	719	1	YMP8_CAEEL	HYPOTHETICAL 82.6 KD P	1.08e-04
25	118	4.3	250	1	CD27_MOUSE	CD27L RECEPTOR PRECURS	1.29e-03
26	113	4.2	415	1	TNRC_MOUSE	LYMPHOTOXIN-BETA RECEP	7.17e-03
27	110	4.1	277	1	CD40_HUMAN	CD40L RECEPTOR PRECURS	1.96e-02
28	109	4.0	1789	1	LMB1_DROME	LAMININ BETA-1 CHAIN P	2.73e-02
29	108	40	3133	1	HMCT_BOMMO	HEMOCYTIN PRECURSOR (H	3.79e-02
30	102	3.8	415	1	BOFH_BRAOL	PUTATIVE TRANSCRIPTION	2.60e-01
31	104	3.8	431	1	SECY_BACSU	PREPROTEIN TRANSLOCASE	1.38e-01
32	104	3.8	569	1	HXT8_YEAST	HEXOSE TRANSPORTER HXT	1.38e-01
33	100	3.7	131	1	NU3M_CANPA	NADH-UBIQUINONE OXIDOR	4.86e-01
34	101	3.7	424	1	LEAF_ARATH	LEAFY PROTEIN.	3.56e-01
35	101	3.7	502	1	K2M3_SHEEP	KERATIN, TYPE II MICRO	3.56e-01
36	100	3.7	549	1	COX1_TRYBB	CYTOCHROME C OXIDASE P	4.86e-01
37	100	3.7	628	1	RA21_SCHPO	DOUBLE-STRAND-BREAK RE	4.86e-01
38	98	3.6	85	1	OE18_NPVOP	OCCLUSION-DERIVED VIRU	8.98e-01
39	99	3.6	269	1	CD40_BOVIN	CD40L RECEPTOR PRECURS	6.6le-01
40	98	3.6	576	1	HXT4_YEAST	LOW-AFFINITY GLUCOSE T	8.98e-01
41	98	3.6	854	1	UBPN_HUMAN	UBIQUITIN CARBOXYL-TER	8.98e-01
42	99	3.6	974	1	MYSB_MESAU	MYOSIN HEAVY CHAIN, CA	6.61e-01
43	98	3.6	1375	1	Y1P9_YEAST	HYPOTHETICAL 156.9 KD	8.98e-01
44	99	3.6	1935	1	MYSB_RAT	MYOSIN HEAVY CHAIN, CA	6.61e-01
45	99	3.6	1935	1	MYSB_HUMAN	MYOSIN HEAVY CHAIN, CA	6.6le-01

ALIGNMENTS

PRT: 323 AA.

STANDARD:

AC	P51867:
DT	01-OCT-1996 (REL. 34, CREATED)
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE	FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
	(APO-1 ANTIGEN) (CD95).
GN	APT1 OR PAS.
OS	BOS TAURUS (BOVINE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA: ARTIODACTYLA.
RN	[1]
RP	SEQUENCE FROM N.A.
	MEDLINE: 96226401.
RX	
RA	YOO J., STONE R.T., BEATTIE C.W.;
RL	DNA CELL BIOL. 15:227-234(1996).
CC	-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC	ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC	RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH- INDUCING
CC	SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC	ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC	CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC	APOPTOSIS. FAS- MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC	INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC	SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC	AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC	-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR	EMBL; U34794; G1262193;
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
K₩	APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
FT	SIGNAL 1 16 POTENTIAL.
FT	CHAIN 17 323 FASL RECEPTOR. DOMAIN 17 170 EXTRACELLULAR (POTENTIAL). TRANSHEM 171 188 POTENTIAL.
	DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
FΤ	TRANSMEM 171 188 POTENTIAL.
FT	DOMAIN 189 323 CYTOPLASMIC (POTENTIAL). DOMAIN 45 163 3 X TNFR-CYS.
FT	REPEAT 45 80 TNFR-CYS 1.
FT	REPEAT 81 124 TNFR-CYS 2. REPEAT 125 163 TNFR-CYS 3.
	DOMAIN 238 306 DEATH DOMAIN.
SQ	SEQUENCE 323 AA; 36445 MW; DA5A2A59 CRC32;

```
8.0%; Score 216; DB 1; Length 323;
                                                                                                                                    FT DOMAIN
                                                                                                                                                           191 335
   Best Local Similarity 32.0%; Pred. No. 6.03e-21;
                                                                                                                                    FT DOMAIN
                                                                                                                                                          47
                                                                                                                                                                 166
                                                                                                                                                                                3 X TNFR-CYS.
  Matches 33: Conservative 24: Mismatches 41: Indels 5: Gaps 5:
                                                                                                                                          REPEAT
                                                                                                                                                            47
                                                                                                                                                                      83
                                                                                                                                                                                   TNFR-CYS 1.
                                                                                                                                    FT
                                                                                                                                    FT
                                                                                                                                           REPEAT
                                                                                                                                                            84
                                                                                                                                                                     127
                                                                                                                                                                                   THER-CYS 2.
          72 RDGDTPECVLCSEGNEYTDKSHHSDKCIRCSICDEEHGLEVEONCTRTRNTKCRCKSNFF 131
                                                                                                                                    FT REPEAT
                                                                                                                                                           128
                                                                                                                                                                     166
                                                                                                                                                                              INFR-CYS 3.
                                                                                                                                           DOMATN
                                                                                                                                                                 314
                                                                                                                                                                                   DEATH DOMAIN.
             FT
                                                                                                                                                           230
          89 RSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGOT-N-KSSCTTTRDTVCOCEKGSF 146
                                                                                                                                    FT
                                                                                                                                           CARROHYD
                                                                                                                                                           118
                                                                                                                                                                     118
                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                          136 136
                                                                                                                                                                                   POTENTIAL.
                                                                                                                                           CARROHYD
                                                                                                                                    SO SECUENCE 335 AA: 37732 MW: 3BF8F973 CRC32:
Db 132 CNSSPCEHCNPC-TTCEHG-I-IEKCTPTSNTKCKGSRSHANS 171
                147 QDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASST 189
RESULT 2
ID FASA_HUMAN
                         STANDARD;
                                             PRT: 335 AA.
       P25445;
AC.
       01-MAY-1992 (REL. 22, CREATED)
       01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
       01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                  To to the test of 
       FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
       (APO-1 ANTIGEN) (CD95 ANTIGEN).
       APT1 OR FAS.
OS
       HOMO SAPIENS (HUMAN).
       EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
                                                                                                                                    RESULT 3
                                                                                                                                    ID TNR2 MOUSE STANDARD; PRT; 474 AA.
                                                                                                                                    AC P25119:
RP
       SECUENCE FROM N.A.
                                                                                                                                           01-MAY-1992 (REL. 22, CREATED)
                                                                                                                                           01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
PY
       MRDLINE: 91309137.
       ITOH N., YONEHARA S., ISHII A., YONEHARA M., MIZUSHIMA S.I.,
                                                                                                                                    DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
       SAMESHIMA M., HASE A., SETO Y., NAGATA S.;
       CELL 66:233-243(1991).
                                                                                                                                          TNFR2 OR TNFR-2.
RT.
       [2]
                                                                                                                                    OS MUS MUSCULUS (MOUSE).
RN
       SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335.
       MEDLINE: 92268122.
       OEHM A., BEHRMANN I., FALK W., PAWLITA M., MAIER G., KLAS C.,
                                                                                                                                    RN
       LI-WEBER M., RICHARDS S., DHEIN J., TRAUTH B.C., PONSTINGL H.,
                                                                                                                                    RP SECUENCE FROM N.A.
       KRAMMER P.H.;
                                                                                                                                    RX MEDLINE: 91187885.
       J. BIOL. CHEM. 267:10709:10715(1992).
                                                                                                                                    RA
RI.
                                                                                                                                           WONG G.H., CHEN E.Y., GOEDDEL D.V.;
PN
       STRUCTURE BY NMR OF 218-335.
                                                                                                                                    RL
       MEDLINE; 97122332.
                                                                                                                                    RN [2]
       HUANG B., EBERSTADT M., OLEJNICZAK E.T., MEADOWS R.P., FESIK S.W.;
                                                                                                                                    RP
                                                                                                                                           SPOURNCE FROM N.A.
       NATURE 384:638-641(1996).
                                                                                                                                    RX MEDLINE; 91246168.
       -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
            ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
                                                                                                                                           COPELAND N.G., JENKINS N.A., SMITH C.A.;
CC
             RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH- INDUCING
                                                                                                                                           MOL. CELL. BIOL. 11:3020-3026(1991).
                                                                                                                                    RL
            SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
                                                                                                                                          [3]
                                                                                                                                    RN
            ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
                                                                                                                                    RP SEQUENCE OF 1-26 FROM N.A.
            CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
                                                                                                                                    RC STRAIN=NOD:
             APOPTOSIS. FAS- MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
                                                                                                                                           JACOB C.O., LIU J.:
            INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
            SUICIDE OF MATURE T-CELLS, OR BOTH.
                                                                                                                                    CC -!- FUNCTION: RECEPTOR FOR THE-ALPHA.
       -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
       -! - DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD.
            AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                           EMBL; M60469; G199828; -.
                                                                                                                                    DR RMBL: M59378: G202095: -.
       -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
       -!- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;
                                                                                                                                    DR EMBL: U39488; G1145885; -.
            WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
                                                                                                                                           PIR: B38634: B38634.
DR EMBL; M67454; G182410; -.
                                                                                                                                          HSSP; P19438; 1TNR.
DR EMBL: X63717: G28742: -.
                                                                                                                                           MGD: MGI:98782: TNFR2.
                                                                                                                                           PROSITE; PS00652; TNFR_NGFR_1; 2.
       PIR: A40036: A40036.
                                                                                                                                    DR
       PIR; S24543; S24543.
                                                                                                                                    DR
                                                                                                                                           PROSITE; PS50050; TNFR_NGFR_2; 3.
     PDB; 1DDF; 12-NOV-97.
                                                                                                                                    KW
DR MIM; 134637; -.
                                                                                                                                          SIGNAL.
                                                                                                                                                            1
       PROSITE; PS00652; TNFR_NGFR_1; 2.
                                                                                                                                    PΨ
                                                                                                                                           CUATM
                                                                                                                                                             23
       PROSITE: PS50050: TNFR NGFR 2: 2.
                                                                                                                                           DOMAIN
                                                                                                                                                             23
                                                                                                                                    FT
                                                                                                                                                                     258
DR PROSITE: PS50017: DEATH DOMAIN: 1.
                                                                                                                                          TRANSMEM 259
                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                     288
KW APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL;
                                                                                                                                    FT
                                                                                                                                           DOMAIN
                                                                                                                                                            289
                                                                                                                                                                     474
       3D-STRUCTURE.
                                                                                                                                           DOMAIN
                                                                                                                                                            39
                                                                                                                                                                     203
                                                                                                                                                                                   4 X TNFR-CYS.
KW
                                                                                                                                    FT
FΤ
       SIGNAL
                                                POTENTIAL.
                                                                                                                                    FT
                                                                                                                                           REPEAT
                                                                                                                                                            39
                                                                                                                                                                                   TNER-CYS 1
    CHAIN
                         17 335
                                           FASI, RECEPTOR.
                                                                                                                                    FT
                                                                                                                                           REPEAT
                                                                                                                                                           78
                                                                                                                                                                  119
                                                                                                                                                                                   TNFR-CYS 2.
FT DOMATN
                         17 173
                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                   TNFR-CYS 3.
                                                                                                                                    PΤ
                                                                                                                                           REPEAT
                                                                                                                                                           120
    TRANSMEM
                     174
                                190
```

```
CYTOPLASMIC (POTENTIAL).
                       7.0%; Score 191; DB 1; Length 335;
 Best Local Similarity 35.1%; Pred. No. 3.59e-16;
 Matches 34: Conservative 21: Mismatches 37: Indels 5: Gaps 4;
       82 CVPCOPGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTONTKCRCKPNFFCNSTVCE 141
         96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGQT-N-KSSCTTTRDTVCQCEKGSFQDKNSPE 153
     142 HCDPC-TKCEHGIIK--ECTLTSNTKCKEEGSRSNLG 175
     154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTG 190
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
    LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
    PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
    GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
    SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
    RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
                               THIMOD MECONSTS PACTOR RECEDEDR 2
                               EXTRACELLULAR (POTENTIAL).
                               CYTOPLASMIC (POTENTIAL).
                   164
203
    REPEAT
               165
                               INFR-CYS 4.
```

```
PT DISULFID
                              BY SIMILARITY.
                                                                                     ID NGFR HUMAN STANDARD:
    DISULFID
                      68
                              BY SIMILARITY.
PT
               55
                                                                                     AC
FT
    DISULFID
               58
                      76
                              BY SIMILARITY.
                                                                                    DТ
    DISULFID
                             BY SIMILARITY.
               70
                      04
                                                                                    DΤ
    DISULFID
              97
                     111
                            BY SIMILARITY.
    DISHLETD
              101
                     119
                              BY SIMILARITY
    DISULFID
              121
                     127
                              BY SIMILARITY.
                                                                                     DE
    DISULFID
                             BY SIMILARITY.
              136
                     145
                                                                                    GN
    DISULFID
             139
                     163
                            BY SIMILARITY.
                                                                                    OS
    DISULFID
              166
                     181
                              BY SIMILARITY.
                                                                                    OC.
FT
FΤ
    CARBOHYD
              69
                      69
                              POTENTIAL.
FT CARBOHYD 195 195
                              POTENTIAL.
SQ SEQUENCE 474 AA; 50319 NW; DC32B2B6 CRC32;
                                                                                     RP
                       7.0%: Score 189: DB 1: Length 474:
 Best Local Similarity 27.6%; Pred. No. 8.49e-16;
 Matches 29; Conservative 27; Mismatches 44; Indels 5; Gaps 5;
      76 CADCEASM-YTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCACEAGRYCALKTHSG 134
                                                                                     CC
        96 CNPCTEGVDYTIASNNLPSCLLCTV-CKSGQTNKSSCTTTRDTVCQCEKGSFQD-KNSPE 153
Qy
                                                                                    CC
                                                                                     CC.
     135 SCROCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTD 179
         154 MCRTC-RTG-CPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAE 196
RESULT 4
    VC22_VARV
                 STANDARD:
                               PRT: 349 AA.
ID
AC
    P34015:
    01-FEB-1994 (REL. 28, CREATED)
    01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
    PROTEIN C22/B28 HOMOLOG.
                                                                                     PΨ
08
    VARIOUA VIDIG
    VIRIDAE: DS-DNA ENVELOPED VIRUSES: POXVIRIDAE: CHORDOPOXVIRINAE:
00
    ORTHOPOXVIRUSES
                                                                                     ΡŤ
                                                                                     FT
    SEQUENCE FROM N.A.
PP
                                                                                     FT
RC
    STRAIN-INDIA-1967 / ISOLATE IND3;
                                                                                     FΤ
ΡY
    MEDLINE; 93202281.
                                                                                     PT
    SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.:
                                                                                     PT
    FEBS LETT. 319:80-83(1993).
    -!- SIMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
    EMBL: X69198; G457087; -.
                                                                                     ΡŤ
    EMBL; X67117; G516449; -.
    PIR: D36858: D36858.
    PIR: $35987: $35987.
                                                                                     FT
    PIR: $46888; $46888.
    HSSP: P19438: 1TNR.
    PROSITE: PS00652: TNFR NGFR 1: 2.
nR
    PROSITE; PS50050; TNFR_NGFR_2; 2.
    REPEAT.
                                                                                     PΨ
FT
    DOMAIN
                31
                    108
                              2 X TNFR-CYS.
ΡT
    REPEAT
               31
                      66
                              TNFR-CYS 1.
               67 108
PT
    REPEAT
                              TNFR-CYS 2.
                                                                                     PΨ
SO SEQUENCE 349 AA: 38189 MW: 50D0B435 CRC32:
                       6.9%; Score 187; DB 1; Length 349;
 Best Local Similarity 37.1%; Pred. No. 2.00e-15;
 Matches 33; Conservative 18; Mismatches 31; Indels 7; Gaps 6;
      65 CTPCGSGT-FTSRNNHLPACLSCNGRCNSNOVETRSCNTTHNRICECSPGYYCLLKGSSG 123
      124 -CKACVSOTKCGIGYG-VSGHTSVGDVIC 150
         Tell al II II II II II II
     154 MCRTC -- RTGCPRGMVKVSNCTPRSDIKC 180
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P08138:
    01-AUG-1988 (REL. 08, CREATED)
    01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
    01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
    LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
    (GP80-LNGFR).
    NGFR.
    HOMO SAPIENS (HUMAN).
    EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA; MAMMALIA;
    EMPHERIA: PRIMATES.
    SEQUENCE FROM N.A.
DY
    MEDLINE: 87051725.
    JOHNSON D., LANAHAN A., BUCK C.R., SEHGAL A., MORGAN C., MERCER E.,
    BOTHWELL M., CHAO M.;
    CELL 47:545-554(1986).
    -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
       NT-3, AND NT-4.
   -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
       BOND FORMATION.
    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
   -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M14764: G189205: -.
DR
    PIR; A25218; GQHUN.
    HSSP: P19438: 1TNR.
DR
    MIM: 162010: -
    PROSITE: PS00652: TNFR NGFR 1: 3.
DR
    PROSITE: PS50050: TNFR NGFR 2: 4.
    PROSITE; PS50017; DEATH_DOMAIN; 1.
    RECEPTOR: NEUROGENESIS: TRANSMEMBRANE: GLYCOPROTEIN; REPEAT;
    PHOSPHORYLATION; SIGNAL.
κw
ΡT
    SIGNAL
                      28
    CHAIN
                      427
                               NGF RECEPTOR.
    DOMAIN
                29
                     250
                               EXTRACELLULAR (POTENTIAL).
    TRANSMEM
                     272
                               POTENTIAL.
               251
    DOMAIN
               273
                      427
                               CYTOPLASMIC (POTENTIAL).
    DOMATN
                31
                     189
                               4 X TNFR-CYS.
    REPEAT
                31
                       65
                               TNFR-CYS 1.
    REPEAT
                66
                     107
                               THER-CYS 2
    REPEAT
               108
                     147
                               TNFR-CYS 3.
    REPEAT
               148
                     189
                               THER-CYS 4
    DOMAIN
               344
                      421
                               DEATH DOMAIN
                               BY SIMILARITY.
    DISULFID
               32
                       43
                       57
                              BY SIMILARITY
    DISULFID
               44
    DISULFID
              47
                       64
                             BY SIMILARITY.
              67
    DISULFID
                       83
                              BY SIMILARITY.
PF.
    DISULFID
              86
89
                       99
                               BY SIMILARITY.
    DISHLETD
                     107
                               BY SIMILARITY.
    DISULFID
              109
                     122
                               BY SIMILARITY.
    DISULFID
              125
                      138
                               BY SIMILARITY.
    DISULFID
               128
                      146
                               BY SIMILARITY
    DISHLETD
              149
                     164
                               BY SIMILARITY.
    DISULFID
               167
                      180
                               BY SIMILARITY.
FT
    DISULFID
               170
                     188
                               BY SIMILARITY.
    DOMATN
               197
                     248
                               SER/THR-RICH.
FT CARBOHYD
               60
                     60
                               POTENTIAL.
SQ SEQUENCE 427 AA; 45183 MW; EE2924BD CRC32;
 Query Match
                        6.8%; Score 185; DB 1; Length 427;
 Best Local Similarity 29.4%; Pred. No. 4.71e-15;
 Matches 25; Conservative 21; Mismatches 37; Indels 2; Gaps 2;
      64 CEPCLDSVTFSDVVSATEPCKPCTECVGLOSMSAPCVEADDAVCRCAYGYYOD-ETTGRC 122
      123 EACRY-CEAGSGLYFSCODKONTVC 146
         156 RTCRTGCPRGMVKVSNCTPRSDIKC 180
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PRT: 427 AA.

٥c

PΤ

FT

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RESULT
ID TNR1_PIG
                   STANDARD:
                                 PRT: 461 AA:
   P50555;
    01-OCT-1996 (REL. 34, CREATED)
    01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
    01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
    TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN
0S
    SUS SCROFA (PIG).
OC.
    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
    EUTHERIA; ARTIODACTYLA.
RN
    SEQUENCE FROM N.A.
RP
RC
    TISSUE=KIDNEY:
    MEDLINE; 96011645.
RX
RA
    SUTER B., PAULI U.H.;
RL
    GENE 163:263-266(1995).
     -!- FUNCTION: RECEPTOR FOR THF-ALPHA, THE ADAPTOR MOLECULE FADD
CC
        RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC
        AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC
        PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
        SUBSECUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC
        PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
    -!- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THER1 LEADS TO
        HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC
        PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC
        WITH THE DEATH DOMAIN OF TRADD, VARIOUS TRADD-INTERACTING
CC
        PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
        TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD, THIS COMPLEX
        ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC
        NF-KAPPA B SIGNALING (BY SIMILARITY).
CC
    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
    -!- SIMILARITY: CONTAINS A LA-NGPR/TNPR-TYPE CYSTEINE-RICH REGION.
    EMBL: U19994: G1141753: -.
DR
    PROSITE: PS00652; TNFR_NGFR_1; 3.
    PROSITE; PS50050; TNFR_NGFR_2; 2.
DR
    PROSITE: PS50017: DEATH DOMAIN: 1.
DR
    RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
KW
ΡT
                  1
                        21
                                POTENTIAL.
PT
    CHAIN
                 22
                       461
                                TUMOR NECROSIS FACTOR RECEPTOR 1.
    DOMAIN
                                EXTRACELLULAR (POTENTIAL).
FT
                 22
                       210
    TRANSMEM
                       233
                                POTENTIAL.
FΤ
                211
FT
    DOMAIN
                234
                       461
                                CYTOPLASMIC (POTENTIAL).
    DOMAIN
                       195
                                4 X TNFR-CYS.
ΡŢ
                 43
    REPEAT
                 43
                        82
                                TNFR-CYS 1.
FF
                       125
FΤ
    REPEAT
                 83
                                TNFR-CYS 2.
                                TNFR-CYS 3.
    REPRAT
                       166
FΤ
                126
FT
    REPEAT
                167
                       195
                                TNFR-CYS 4.
    DOMATN
                362
                       447
                                DEATH DOMAIN
FT
    DISHLEID
                        58
                                BY SINILARITY.
Ρī
                44
PΨ
    DISHLEID
                59
                        72
                                BY SIMILARITY
    DISULFID
                                BY SIMILARITY.
FT
                62
                        81
                        99
                                BY SIMILARITY.
    DISULFID
                84
FT
FT
    DISULFID
                102
                       117
                                BY SIMILARITY.
    DISULFID
                105
                       125
                                 BY SIMILARITY.
FT
    DISULFID
                127
                       143
                                BY SIMILARITY
    DISHLEID
                       158
                                BY SIMILARITY.
                146
FT
    DISULFID
                149
                       166
                                BY SIMILARITY.
PΨ
    DISULFID
                168
                       179
                                BY SIMILARITY.
    DISULFID
                182
                       190
                                 BY SIMILARITY.
FT
FT
    DISULFID
                185
                       194
                                 BY SIMILARITY.
FT
    CARBOHYD
                54
                        54
                                POTENTIAL.
    CARBOHYD
                86
                        86
                                POTENTIAL.
FF
    CARBOHYD
               145
                      145
                                 POTENTIAL.
    CARBOHYD
                151
                      151
                                POTENTIAL.
    SEQUENCE 461 AA; 50696 MW; 8E2C350A CRC32;
                        6.8%; Score 184; DB 1; Length 461;
 Best Local Similarity 36.3%; Pred. No. 7.22e-15;
 Matches 33; Conservative 17; Mismatches 32; Indels 9; Gaps 7;
       81 CRECDNGT-FTASENHLTQCLSCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYR-KYWSE 138
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139 TLFQCLNCSL-CPNGTVQLP-CLEKQDTICN 167
          154 -M--CRTCRTGCPRGMVKVSNCTPRSDIKCK 181
RESULT
                                 PRT; 326 AA.
ID VT2 MYXVL
                  STANDARD:
   P29825:
    01-APR-1993 (REL. 25, CREATED)
    01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DΤ
DΤ
    TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN
OS
    MYXOMA VIRUS (STRAIN LAUSANNE).
    VIRIDAE: DS-DNA ENVELOPED VIRUSES: POXVIRIDAE: CHORDOPOXVIRINAE;
    LEPORIPOVIRUSES.
RN
RP
    SEQUENCE FROM N.A.
RX MEDLINE: 91335768.
    UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
RA
    VIROLOGY 184:370-382(1991).
RI.
CC
    -!- FUNCTION: BINDS TO THE-ALPHA AND BETA, PROBABLY PREVENTS THE TO
CC
        REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC
        ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR
    EMBL: M95181: G332310: -.
DR EMBL: A23729: E199442: -.
DR
    PIR; A40566; GQVZML.
DR
    HSSP: P19438: 1TNR.
DΡ
    PROSITE; PS00652; TNFR_NGFR_1; 2.
    PROSITE; PS50050; TNFR_NGFR_2; 2.
    RECEPTOR; GLYCOPROTEIN; REPEAT: SIGNAL.
KM
FT
    STGNAL
                 1
                       16
                                POTENTIAL.
    CHAIN
                                PROTEIN T2
ΡT
                 17
                      326
    DOMAIN
                                4 X TNFR-CYS.
PT
                 27
                      186
    REPEAT
                                TNFR-CYS 1
FT
                27
                       62
FT
    REPRAT
                 63
                      104
                                TNFR-CYS 2
    DPDPAT
                105
                      147
                                TNFR-CYS 3.
    REPEAT
                148 186
                                TNFR-CYS 4
FT
    CARBOHYD
                66
                       66
                                POTENTIAL.
FT
    CARBOHYD
                181
                      181
                                POTENTIAL.
FT
    CARBOHYD
               205
                    205
                                POTENTIAL.
PT
    CARBOHYD
               238 238
                                POTENTIAL
SQ SEQUENCE 326 AA; 35208 MW; 2F059A61 CRC32;
                        6.6%; Score 180; DB 1; Length 326;
 Best Local Similarity 34.4%; Pred. No. 3.95e-14;
 Matches 31: Conservative 20: Mismatches 34: Indels 5: Gaps 4:
      61 CSPCKNET-FTASTNHAPACVSCRGRCTGHLSESQSCDKTRDRVCDCSAGNYCLLKGQEG 119
      Db
     120 CRICAPKTKCPAGYG-VSGHTRTGDVLCTK 148
     || | : | || | || | : |: |:
155 CRTC--RTGCPRGMVKVSNCTPRSDIKCKN 182
RESULT 8
    FASA_MOUSE
                STANDARD:
                                 PRT: 327 AA.
ID
   P25446;
    01-MAY-1992 (REL. 22, CREATED)
    01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
    01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
    FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE
    (APO-1 ANTIGEN) (CD95).
GN
    APT1 OR PAS.
OS
    MUS MUSCULUS (MOUSE).
    EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA; MAMMALIA;
    EUTHERIA; RODENTIA.
00
RN
    111
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96 CNPCTEGYDYTIASNNLPSCLLCTVCKS--GOTNKSSCTTTRDTVCQCEKGSFQDKNSPE 153

9

P19438:

TNR1 HUMAN STANDARD:

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RP SEQUENCE FROM N.A.
RX
     MEDLINE: 92148151.
                                                                                           RESULT
    WATANABE-FUKUNAGA R., BRANNAN C.I., ITOH N., YONEHARA S.,
                                                                                           ID
    COPELAND N.G., JENKINS N.A., NAGATA S.:
     J. IMMUNOL. 148:1274-1279(1992).
RN
     SEQUENCE OF 1-96 FROM N.A.
RP
     MEDLINE; 93189576.
RΑ
     ADACHI M., WATANABE-FUKUNAGA R., NAGATA S.;
     PROC. NATL. ACAD. SCI. U.S.A. 90:1756-1760(1993).
RL
RN
     [3]
RP
     VARTANT LPR.
RX
     MEDLINE: 92195401.
     WATANABE-FUKUNAGA R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,
RA
RA
RL
     NATURE 356:314-317(1992).
CC
     -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC
        ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
        RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH- INDUCING
CC
CC
        SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC
        ACTIVATION, ACTIVE CASPASE-8 INITIATES THE SUBSECUENT CASCADE OF
CC
        CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
        APOPTOSIS. FAS- MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
cc
         INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC
        SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC
     -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
     -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC
        LIVER, LUNG, HEART, AND ADULT OVARY.
CC
     -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC
        AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC
     -!- DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC
        DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC
        PRODUCTION.
     -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
     RMBL; M83649; G193226; -.
     EMBL: $56490: G298506:
     EMBL; $56485; G298506; JOINED.
     EMBL; $56486; G298506; JOINED.
     PIR; A46484; A46484.
ΠP
     HSSP: P19438: 1TNR.
DR
    MGD; MGI:95484; FAS.
DR
     PROSITE; PS00652; TNFR_NGFR 1; 2.
     PROSITE: PS50050: TNFR NGFR 2: 2.
DR
     PROSITE: PS50017: DEATH DOMAIN: 1.
KW
     APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL;
     DISEASE MUTATION.
FT
     STGNAL
                 1
FT
     CHAIN
                 22
                       327
                                FASL RECEPTOR.
     DOMAIN
PT
                 22
                       169
                                 EXTRACELLULAR (POTENTIAL).
     TRANSMEM
                170
                       186
                                POTENTIAL.
     DOMATH
FT
                187
                       327
                                CYTOPLASMIC (POTENTIAL).
     DOMATN
                 43
                       162
                                3 X TNFR-CYS.
     PEDEAT
                 43
                        79
                                TNER-CYS 1.
     REPEAT
                 80
                       123
                                TNFR-CYS 2.
PΨ
     REPEAT
                       162
                124
                                TNFR-CYS 3.
     DOMAIN
                222
                       306
                                 DEATH DOMAIN.
     CARBOHYD
                        43
                                 POTENTIAL.
PΤ
                 43
     CARBOHYD
               114
                       114
                                POTENTIAL.
    VARIANT
                246
                       246
                                I -> N (IN LPR).
   SEQUENCE 327 AA; 37418 MW; 22D6DC39 CRC32;
                         6.5%; Score 177; DB 1; Length 327;
  Best Local Similarity 30.5%; Pred. No. 1.40e-13;
           29; Conservative 25; Mismatches 36; Indels 5; Gaps 5;
       75 TPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTONTKCKCKPDFYCDSP 134
          93 TGACNPCTEGVDYTIASNNLPSCLLCTVCKSGOT-N-KSSCTTTRDTVCOCEKGSFODKN 150
      135 GCEHCVRC-ASCEHGTLE-P-CTATSNTNCRKOSP 166
          a El Fred el a la Halla desde
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151 SPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESA 185

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01-FEB-1991 (REL. 17, CREATED)
DΤ
     01-PEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DΨ
     01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
    TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DR
   BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).
GN
     TNFR1 OR TNFAR.
     HOMO SAPIENS (HUMAN).
OS
     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC.
     EUTHERIA: PRIMATES.
RN
RР
     SEQUENCE FROM N.A.
    TISSUE=PLACENTA;
RC
RX
     MEDLINE: 90235285.
RA
     SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
    GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RA
     CELL 61:361-370(1990).
RN
     [2]
RP
     SEQUENCE FROM N.A.
RX
    MEDLINE: 90235284.
     LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
PΑ
RA
     TABUCHI H., LESSLAUER W.;
     CELL 61:351-359(1990).
RL
RN
     [3]
ВÞ
     SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RY
     MEDLINE: 91006021.
RΑ
     NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
     ADERKA D., HOLTMANN H., WALLACH D.;
RL
     EMBO J. 9:3269-3278(1990).
RN
PD
     SEQUENCE FROM N.A.
RX
     MEDLINE; 91090841.
RA
     HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA
     LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
     DNA CELL BIOL, 9:705-715(1990).
Rf.
PN
RP
     SEQUENCE FROM N.A.
RC
    TISSUE-PLACENTA:
PY
    MEDLINE: 91017509.
     GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RL
     PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).
RN
ВÞ
     SPOTTENCE FROM N A
RX
    MEDLINE; 92250049.
     FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;
RA
RL
     GENOMICS 13:219-224(1992).
RN
     [7]
RP
     SEQUENCE OF 41-45.
ВX
     MEDLINE: 90110215.
    ENGELMANN H., NOVICK D., WALLACH D.;
RΑ
Rt.
    J. BIOL. CHEM. 265:1531-1536(1990).
RN
RP
     X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX
    MEDLINE: 93258809.
     BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA
     BROGER C., LOETSCHER H., LESSLAUER W.;
     CELL 73:431-445(1993).
RT.
RN
     [9]
     X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RP
    MEDLINE; 97094982.
RX
RA
     NAISMITH J.H., DEVINE T.Q., KHONO H., SPRANG S.R.;
     STRUCTURE 4:1251-1262(1996).
     -! - FUNCTION: RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE PADD
cc
CC
         RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC
         AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC
         PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC
         SUBSECUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC
         PROTEASES) MEDIATING APOPTOSIS.
     -! - SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THER! LEADS TO
         HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
```

PRT: 455 AA.

RESULT 10

```
CC
CC
CC
CC
        PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
        WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
        PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
        TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
        ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC
        NF-KAPPA B SIGNALING.
CC
    · I · SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
    EMBL: X55313: G37224: -.
DR
DR
    EMBL; M33294; G339745; -.
    EMBL: M58286: G339754:
    EMBL; M63121; G339756; -.
DR
    EMBL; M75866; G339750;
DR
    EMBL: M75864: G339750: JOINED.
    EMBL: M75865; G339750; JOINED.
DR
    EMBL; M60275; G339760; -.
    EMBL; A21522; G579600; -.
DR
    PIR; A34899; GQHUT1.
DR
    PIR: A35010: A35010.
DR
    PIR: S12057; S12057.
    PIR: A38208: A38208
DR
    PDB; 1TNR; 31-JUL-94
    PDB; 1NCF; 07-DEC-95.
    PDB; 1EXT; 11-JAN-97.
DR
DR
    MIM; 191190; -
    PROSITE: PS00652: TNFR NGFR 1: 3.
DR
    PROSITE; PS50050; TNFR_NGFR_2; 3.
DR
    PROSITE: PS50017: DEATH DOMAIN: 1.
    RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;
KW
ĸW
    3D-STRUCTURE.
    SIGNAL
FT
RΨ
    CHAIN
                22
                      455
                                TUMOR NECROSIS FACTOR RECEPTOR 1.
    CHAIN
                                TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
RΨ
                41
                      291
    DOMAIN
                22
                      211
                                EXTRACELLULAR (POTENTIAL).
    TRANSMEM
               212
                      234
                                POTENTIAL.
FT
    DOMAIN
                235
                      455
                               CYTOPLASMIC (POTENTIAL).
                      196
    DOMATN
                               4 X TNFR-CYS.
PT
                43
FT
    DEDEAT
                43
                       82
                               TNFR-CYS 1.
FT
    REPEAT
                83
                      125
                               TNFR-CYS 2.
FT
    REPEAT
               126
                      166
                               TNFR-CYS 3.
FT
    REPEAT
               167
                      196
                               TNFR-CYS 4.
FT
    DOMAIN
               356
                      441
                               DEATH DOMAIN.
FT
    DISULFID
                44
                       58
                       72
    DISULFID
PΨ
               59
    DISULFID
FT
               62
                       81
PΤ
    DISULPID
                84
                       99
FT
    DISULFID
               102
                      117
    DISULFID
FT
               105
                      125
    DISULFID
               127
                      143
RT
    DISULFID
               146
                      158
FT
    DISULFID
               149
                      166
    DISULFID
               168
                      179
FT
    DISULFID
FT
               182
                      191
FT
    DISHLETD
               185
                      195
FT
    CARBOHAD
                54
                       54
                                POTENTIAL.
    CARBOHYD
                      145
                                POTENTIAL.
               145
FΤ
    CARBOHYD
               151
                      151
                                POTENTIAL.
    CONFLICT
               412
                      412
                                MISSING (IN REF. 4).
                                GPAA -> APP (IN REF. 4).
PT
    CONFLICT
              443
                     446
   SEQUENCE 455 AA; 50494 MW; CEOEAOGF CRC32;
                        6.4%; Score 173; DB 1; Length 455;
 Best Local Similarity 37.1%; Pred. No. 7.47e-13;
 Matches 33; Conservative 12; Mismatches 37; Indels 7; Gaps 6;
      81 CRECESG-SFTASENHLRHCLSCSKCRKEMGOVEISSCTVDRDTVCGCRKNQYRHYWSEN 139
         96 CNPCTEGVDYTIASNNLPSCLLCTVC-KS-GQTNKSSCTTTRDTVCQCEKGSFODKNSPE 153
     140 LFQCFNCSL-CLNGTVHLS-CQEKQNTVC 166
        154 M -- CRTCRTGCPRGMVKVSNCTPRSDIKC 180
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ID NGFR CHICK STANDARD:
                                 PRT: 416 AA.
AC P18519;
DT
    01-NOV-1990 (REL. 16, CREATED)
    01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
    01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE
GN
    NGFR
OS
    GALLUS GALLUS (CHICKEN).
    EUKARYOTA; METAZOA; CHORDATA: VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC.
00
     GALLIFORMES.
RN
    SEQUENCE FROM N.A.
RP
    TISSUE=BRAIN:
RC
RX
    MEDLINE: 90166579
    LARGE T.H., WESKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,
     SHOOTER E.M., REICHARDT L.F.;
RA
     NEURON 2:1123-1134(1989).
RL
RN
RP
    SECUENCE OF 21-416 FROM N.A.
    MEDLINE; 90152140.
RA
    HEUER J.G., FATEMIE-NAINIE S., WHEELER E.F., BOTHWELL M.;
RL
    DEV. BIOL. 137:287-304(1990).
    -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC
        NT-3, AND NT-4.
     -! - SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC
       BOND FORMATION.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR PIR: JN0006: JN0006.
DR PIR: A60504: A60504.
DR
    PROSITE: PS00652: TNFR NGFR 1: 3.
    PROSITE; PS50050; TNFR_NGFR_2; 3.
DR
    PROSITE: PS50017: DEATH DOMAIN: 1.
DR
    RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW
KW
    PHOSPHORYLATION: SIGNAL.
FΤ
    STGNAT.
                 1
                       19
                                DOTENTIAL.
                                NGF RECEPTOR.
    CHAIN
    DOMAIN
                                EXTRACELLULAR (POTENTIAL).
FT
                 29 239
    TRANSMEM
                240
                       261
                                POTENTIAL
                     416
                               CYTOPLASMIC (POTENTIAL).
FT
    DOMATN.
                262
    DOMAIN
                       181
                                4 X TNFR-CYS.
FT
                23
FT
    REPEAT
                 23
                       57
                                TNFR-CYS 1.
                                TNFR-CYS 2
                       100
FT
    REPEAT
                 58
    REPEAT
                101
                     140
                                TNFR-CYS 3.
PP
ΡT
    REPEAT
                141
                       181
                                THER-CYS 4.
FT
    DOMAIN
                188
                       236
                                SER/THR-RICH
ΡT
    DOMAIN
                333
                       410
                                DEATH DOMAIN
PΨ
    DISULFID
                24
                                BY SIMILARITY
    DISULFID
                        49
                                BY SIMILARITY.
PT
                 36
FT
    DISULFID
                 39
                        56
                                BY SIMILARITY
                       75
                                BY SIMILARITY.
    DISULFID
                 59
PT
    DISULFID
                 78
                       91
                                BY SIMILARITY
FT
                                BY SIMILARITY
FΤ
    DISULFID
                 81
                       99
ΡT
    DISULFID
                101
                       114
                                BY SIMILARITY
    DISULFID
               117
                      130
                                BY SIMILARITY.
FT
    DISULFID
                120
                     138
                                BY SIMILARITY.
FT
PT
    DISULPTD
                141
                       156
                                BY SIMILARITY.
FT
    DISULFID
                159
                      172
                                BY SIMILARITY.
    DISULFID
               162 180
                                BY SIMILARITY.
PT
FT
    CARBOHYD
                 52
                       52
                                POTENTIAL.
27
    CONFLICT
                 36
                       36
                                C -> Y (IN REF. 2).
                     173
FT
    CONFLICT
                173
                                T -> K (IN REF. 2).
FT CONFLICT
               276
                     276
                                N -> S (IN REF. 2).
                                K -> R (IN REF. 2).
               396 396
FT CONFLICT
SO SEQUENCE 416 AA: 44654 MW: 4D3F086A CRC32:
                         6.3%: Score 170: DB 1: Length 416:
  Best Local Similarity 30.6%; Pred. No. 2.60e-12;
  Matches 26; Conservative 17; Mismatches 40; Indels 2; Gaps 2;
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56 CEPCLDSVTYSDTVSATEPCKPCTQCVGLHSMSAPCVESDDAVCRCAYGYFODELSGS-C 114
         96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGOTNKSSCTTTRDTVCQCEKGSFQDKNSPEMC 155
      115 KECSI-CEVGFGLMFPCRDSQDTVC 138
          :1 1 1 : 1 4 1
      156 RTCRTGCPRGMVKVSNCTPRSDIKC 180
RESULT 11
ID NGFR RAT
                   STANDARD;
                                  PRT; 425 AA.
     P07174:
ŊΤ
     01-APR-1988 (REL. 07, CREATED)
     01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
     01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
     LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE
GN
     NGFR.
OS
     RATTUS NORVEGICUS (RAT).
œ
     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
     EUTHERIA; RODENTIA.
RN
     SEQUENCE FROM N.A.
RP
RX
     MEDLINE: 87115859.
     RADEKE M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;
     NATURE 325:593-597(1987).
RP
     SEQUENCE OF 1-22 FROM N.A.
RC
     TISSUE=LIVER:
     MEDLINE: 93077038.
     METSIS M., TIMMUSK T., ALLIKMETS R., SAARMA M., PERSSON H.;
RT.
     GENE 121:247-254(1992).
RN
     STRUCTURE BY NMR OF 334-418.
RA
     LIEPINSH E., ILAG L., OTTING G., IBANEZ C.;
     SUBMITTED (JAN-1997) TO THE PDB DATA BANK.
     -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BONF,
CC
     -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
        BOND FORMATION.
     -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
     -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
ΠŔ
     EMBL; X05137; G56756; -.
     EMBL; X61269; -; NOT_ANNOTATED_CDS.
     PIR; A26431; A26431.
     PDB; 1NGR; 29-JUL-97.
ΠP
    PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 4.
     PROSITE; PS50017; DEATH_DOMAIN; 1.
     RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW
     PHOSPHORYLATION; SIGNAL; 3D-STRUCTURE.
FT
     SIGNAL
                  1
                       29
FT
     CHAIN
                 30
                       425
                                 NGF RECEPTOR.
ΡŢ
     DOMAIN
                 30
                       251
                                 EXTRACELLULAR (POTENTIAL).
PΨ
     TRANSMEM
                252
                       273
                                 POTENTIAL.
FT
     DOMAIN
                274
                       425
                                 CYTOPLASMIC (POTENTIAL).
     DOMATN
                 32
                       190
                                 4 X TNFR-CYS.
     REPEAT
                 32
                        66
                                 TNFR-CYS 1.
     REPEAT
                 67
                       108
                                 TNFR-CYS 2.
FT
     REPEAT
                109
                       148
                                 TNFR-CYS 3.
PΨ
     DEDENT
                149
                       190
                                 TNFR-CYS 4.
     DOMAIN
                198
                       249
                                 SER/THR-RICH
     DOMATN
PΨ
                354
                       419
                                 DEATH DOMAIN
     DISULFID
                33
                                 BY SIMILARITY.
     DISULFID
                45
                        58
                                 BY SIMILARITY.
FT
     DISULFID
                 48
                        65
                                 BY SIMILARITY.
FT
     DISULFID
                 68
                        84
                                 BY SIMILARITY.
     DISULFID
                 87
                       100
                                 BY SIMILARITY
FT
     DISULFID
                 90
                       108
                                 BY SIMILARITY.
FT
     DISULFID
                110
                       123
                                 BY SIMILARITY.
    DISULFID
                126
                       139
                                 BY SIMILARITY.
```

```
FT DISULFID
                                BY SIMILARITY.
                                BY SIMILARITY
ΡT
    DISULFID
               150
                      165
ΡT
    DISULPID
                168
                       181
                                BY SIMILARITY.
FT
    DISULFID
                171
                      189
                                BY SIMILARITY.
    CARBOHYD
               61
                      61
                                POTENTIAL.
                                POTENTIAL
    CARBOHYD
                       71
                71
   SEQUENCE
               425 AA; 45432 MW; 7D78F258 CRC32;
                        6.3%; Score 171; DB 1; Length 425;
  Best Local Similarity 28.2%; Pred. No. 1.72e-12;
  Matches 24; Conservative 20; Mismatches 39; Indels 2; Gaps 2;
       65 CEPCLDNVTFSDVVSATEPCKPCTECLGLOSMSAPCVEADDAVCRCAYGYYODEETGH-C 123
          96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGOTNKSSCTTTRDTVCOCEKGSFODKNSPEMC 155
     124 EACSV-CEVGSGLVFSCODKONTVC 147
          31 | 1 | 131 : : 1
     156 RTCRTGCPRGMVKVSNCTPRSDIKC 180
RESULT 12
ID VT2_SFVKA
                  STANDARD:
                                 PRT: 325 AA.
   P25943:
    01-MAY-1992 (REL. 22, CREATED)
    01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DΤ
    TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN
OS
     SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).
ന
    VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
00
    LEPORIPOVIRUSES.
RN
    [1]
RP
     SECUENCE FROM N.A.
PΧ
    MEDLINE; 87321103.
     UPTON C., DELANGE A.M., MCFADDEN G.;
    VIROLOGY 160:20-30(1987).
RT.
RN
RP
    FUNCTION.
    MEDLINE: 91207415.
    SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,
RA
    MCFADDEN G., GOODWIN R.G.;
    BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).
    -!- FUNCTION: BINDS TO THE ALPHA AND BETA. PROBABLY PREVENTS THE TO
CC
        REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC
        ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC
   -! SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; M17433; -; NOT_ANNOTATED_CDS.
DR
    EMBL: A23727: E199408: -.
    PIR: B43692; B43692.
DR
    HSSP: P19438: 1TNR.
    PROSITE; PS00652; TNFR_NGFR_1; 2.
DR
    PROSITE: PS50050: TNFR_NGFR_2; 1.
    RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
KW
                       16
                                POTENTIAL.
                                PROTEIN T2
ΡT
    CHAIN
                 17
                       325
ΡŢ
    DOMATN
                 27
                       186
                                4 X TNFR-CYS.
FT
     REPEAT
                27
                       62
                                TNFR-CYS 1.
FΨ
     REPEAT
                63
                      104
                                TNFR-CYS 2
FΤ
     REPEAT
                105
                       147
                                TNFR-CYS 3.
PΨ
    REPEAT
                148
                       186
                                TNER-CYS 4.
PΨ
    CARBOHYD
               105
                       105
                                POTENTIAL.
FT
    CARBOHYD
                181
                       181
                                POTENTIAL
FΨ
    CARBOHYD
                205
                       205
                                POTENTIAL.
                238
                      238
                                POTENTIAL.
FT
    CARBOHYD
SO SEQUENCE 325 AA; 35132 MW; C9D2C87B CRC32;
 Query Match 6.1%; Score 166; DB 1; Length 325; Best Local Similarity 33.0%; Pred. No. 1.36e-11;
  Matches 29; Conservative 20; Mismatches 34; Indels 5; Gaps 4;
       61 CSPCEDGT-FTASTNHAPACVSCRGPCTGHLSESOPCDRTHDRVCNCSTGNYCLLKGQNG 119
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, ., ,

```
SO SEQUENCE 461 AA: 50969 MW: 82F68B08 CRC32;
      96 CNPCTEGVDYTIASNNLPSCLLC-TVCKSGOTNKSSCTTTRDTVCOCEKGSFODKNSPEM 154
                                                                                             Query Match 5.9%; Score 159; DB 1; Length 461; Best Local Similarity 30.0%; Pred. No. 2.35e-10;
    120 CRICAPQTKCPAGYG-VSGHTRAGDTLC 146
         TEL 31 II 3 II 1 31 I
      155 CRTC--RTGCPRGMVKVSNCTPRSDIKC 180
                                                                                             Matches 27; Conservative 16; Mismatches 40; Indels 7; Gaps 6;
                                                                                                  81 CEVCDKGT-FTASQNHVRQCLSCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSET 139
                                                                                                RESULT 13
                                 PRT: 461 AA.
    TNR1 RAT
                   STANDARD:
     P22934:
                                                                                           Db 140 HFOCVDC-SPCFNGTVTIP-CKEKONTVCN 167
     01-AUG-1991 (REL. 19, CREATED)
                                                                                                        1 4 : 1 1 1 :: 1 :: 1:
DΤ
     01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
                                                                                               153 EM-CRICRIGCPRGMVKVSNCTPRSDIKCK 181
     01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN TMFR1 OR TMFR-1.
                                                                                           RESULT 14
0S
     RATTUS NORVEGICUS (RAT).
     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                           ID TNR2 HUMAN STANDARD:
                                                                                                                             PRT: 461 AA.
oc
     EUTHERIA: RODENTIA.
                                                                                           AC P20333;
                                                                                           DT 01-FEB-1991 (REL. 17, CREATED)
RN
                                                                                           DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
RP
     SEQUENCE FROM N.A.
     MEDLINE: 91090841.
                                                                                           DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
RX
                                                                                           DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
     HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
                                                                                                BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B).
     LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
                                                                                           DE
RA
RL
     DNA CELL BIOL. 9:705-715(1990).
                                                                                           GN TNFR2 OR TNFBR.
     -!- FUNCTION: RECEPTOR FOR THE-ALPHA, THE ADAPTOR MOLECULE FADD
                                                                                           OS HOMO SAPIENS (HUMAN).
CC
                                                                                           OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC
         RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
                                                                                                EUTHERIA: PRIMATES.
CC
         AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC
         PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
                                                                                           PN
         SUBSECUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
                                                                                           RP SEQUENCE FROM N.A.
                                                                                           RX MEDLINE: 90260639.
cc
         PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
                                                                                                SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,
CC
     -!- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THER1 LEADS TO
                                                                                           RA
                                                                                                DOWER S.K., COSMAN D., GOODWIN R.G.;
CC
         HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC
         PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
                                                                                                SCIENCE 248:1019-1023(1990).
cc
         WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
                                                                                           DN
                                                                                                [2]
CC
         PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
                                                                                           RP
                                                                                                SECUENCE FROM N.A.
CC
         THER1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
                                                                                           RX MEDLINE; 91045991.
                                                                                                KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,
cc
         ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
                                                                                                HALE K.K., SQUIRES C.H., THOMPSON R.C., VANNICE J.L.;
CC
         NF-KAPPA B SIGNALING (BY SIMILARITY).
                                                                                           RA
                                                                                                PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).
CC
     -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                           RI.
cc
     -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                           RN [3]
    EMBL; M63122; G207362; -.
                                                                                           RP
                                                                                                SPOTENCE FROM N.A.
                                                                                                MEDLINE: 96299745.
DR
     PIR: B36555; B36555.
                                                                                           PY
                                                                                                BELTINGER C.P., WHITE P.S., MARIS J.M., SULMAN E.P., JENSEN S.J.,
DR
     HSSP: P19438: 1TNR.
DR PROSITE: PS00652: TNFR NGFR 1: 3.
                                                                                                LEPASLIER D., STALLARD B.J., GOEDDEL D.V., DESAUVAGE F.J.,
     PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                BRODEUR G.M.;
DR
                                                                                           RA
     PROSITE: PS50017: DEATH DOMAIN: 1.
                                                                                                GENOMICS 35:94-100(1996).
DR
                                                                                           RI.
     RECEPTOR: TRANSMEMBRANE: GLYCOPROTEIN: REPEAT: SIGNAL: APOPTOSIS.
KW
                                                                                           RN
ΡĪ
     STONAT.
                1
                       21
                               POTENTIAL.
                                                                                           RP
                                                                                                SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
                                                                                           DY
                                                                                                MEDLINE: 90349572.
                                 TUMOR NECROSIS FACTOR RECEPTOR 1.
PΫ
     CHAIN
                       455
                                                                                                HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,
     DOMATN
                 22
                       211
                                 EXTRACELLULAR (POTENTIAL).
                                                                                           RA
ΡT
PΤ
     TRANSMEM 212
                       234
                                POTENTIAL.
                                                                                           RA
                                                                                                RINGOLD G.M.:
                                                                                                PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).
     DOMAIN
                235
                       461
                               CYTOPLASMIC (POTENTIAL).
                                                                                           RL
PТ
     DOMAIN
                       196
                                4 X TNFR-CYS.
                                                                                           RN
FT
                 43
FT
     REPEAT
                 43
                        82
                                 TNFR-CYS 1.
                                                                                           RP
                                                                                                SECUENCE OF 27-31.
     REPEAT
                       125
                                TNFR-CYS 2.
                                                                                                MEDLINE: 90110215.
                 83
FT
     REPEAT
                126
                       166
                                TNFR-CYS 3.
                                                                                           RA
                                                                                                ENGELMANN H., NOVICK D., WALLACH D.;
FT
                                                                                                J. BIOL. CHEM. 265:1531-1536(1990).
     REPEAT
                167
                       196
                                                                                           RL
PΨ
                                 THER-CYS 4.
FT
     DOMAIN
                363
                       448
                                 DEATH DOMAIN
                                                                                           DN
     DISULFID
                 44
                        58
                                 BY SIMILARITY
                                                                                                SECUENCE OF 22-40: 65-69: 136-141: 300-306 AND 346-362.
FT
                                                                                                MEDITINE: 91056048.
     DISULFID
                59
                        72
                                 BY SIMILARITY.
                                                                                           RY
FT
                                                                                                LOETSCHER H., SCHLAEGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,
     DISULPED
                62
                        81
                                 BY SIMILARITY.
FT
                                                                                                BROCKHAIIS M .
FT
     DISULFID
                 84
                        99
                                 BY SIMILARITY.
                                                                                           RA
     DISULFID
                       117
                                 BY SIMILARITY.
                                                                                           RL
                                                                                                J. BIOL, CHEM. 265:20131-20138(1990).
FΤ
                102
     DISULFID
                105
                       125
                                 BY STMILARITY
                                                                                           RN
FT
FT
     DISULFID
                127
                       143
                                 BY SIMILARITY.
                                                                                           RP
                                                                                                CHARACTERIZATION.
                                                                                                MEDLINE: 93016040.
     DISULFID
                146
                       158
                                 BY SIMILARITY.
                                                                                           RY
PT
     DISULPID
                149
                       166
                                 BY SIMILARITY.
                                                                                                PENNICA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,
FT
                                                                                                LIPARI M.T., GOEDDEL D.V.;
     DISULFID
                                 BY SIMILARITY.
FΤ
                168
                       179
FT
     DISULFID
                182
                       191
                                 BY STMILARITY.
                                                                                           RL
                                                                                                J. BIOL. CHEM. 267:21172-21178(1992).
                                                                                               -! - FUNCTION: RECEPTOR FOR THE -ALPHA, HIGH AFFINITY FOR THA-ALPHA AND
FΤ
     DIGHTETD
                185
                       195
                                 DV CIMILADIAN
                                                                                           cc
                                                                                                    APPROXIMATELY 5-FOLD LOWER AFFINITY FOR THF-BETA.
     CARBOHYD
                54
                        54
                                 POTENTIAL.
                                                                                           CC
                                 POTENTIAL.
                                                                                           .00
                                                                                                -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
     CARROHYD
                151
                       151
FΤ
                                                                                                -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
    CARBOHYD
                201
                       201
                                 POTENTIAL.
```

```
LEVEL ON THREONINE RESIDUES.
                                                                                         GN TNFR1 OR TNFR-1.
CC
    -!- SIMILARITY: CONTAINS A LA-NGER/THER-TYPE CYSTEINE-RICH REGION.
                                                                                         OS
                                                                                              MUS MUSCULUS (MOUSE).
    EMBL; M32315; G189186; -.
                                                                                         OC.
                                                                                              EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
    EMBL: M35857: G339752: -.
                                                                                              EUTHERIA; RODENTIA.
    EMBL; U52165; G1469541; -
    EMBL; U52156; G1469541; JOINED.
                                                                                         RP SECUENCE FROM N A
    EMBL; U52157; G1469541; JOINED.
                                                                                         RX
                                                                                              MEDLINE: 91187885.
    EMBL; U52158; G1469541; JOINED.
                                                                                         RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
    EMBL; U52159; G1469541; JOINED.
                                                                                              WONG G.H., CHEN E.Y., GOEDDEL D.V.;
    EMBL: U52160: G1469541: JOINED.
                                                                                         RI.
                                                                                              PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
    EMBL: U52161: G1469541: JOINED.
                                                                                         RN
    EMBL; U52162; G1469541; JOINED.
                                                                                              SEQUENCE FROM N.A.
    EMBL; U52163; G1469541; JOINED.
                                                                                              MEDLINE: 91246168.
                                                                                         RX
    EMBL; U52164; G1469541; JOINED.
                                                                                              GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
    EMBL: M55994; G339758; -.
                                                                                              COPELAND N.G., JENKINS N.A., SMITH C.A.;
    PIR: A35356: A35356.
                                                                                          RL MOL. CELL. BIOL. 11:3020-3026(1991).
DR
    PIR: A36007: A36007.
                                                                                          RN [3]
    PIR: A36475: A36475.
                                                                                         RP
                                                                                              SEQUENCE FROM N.A.
    PIR; B35010; B35010.
                                                                                         RX MEDLINE; 91285014.
                                                                                              BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
    PIR; A23666; A23666.
    HSSP: P19438: 1TNR.
                                                                                              GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
DR
    MIM: 191191: -
                                                                                         RL
                                                                                              EUR. J. IMMUNOL. 21:1649-1656(1991).
DR PROSITE: PS00652: TNFR NGFR 1: 2.
                                                                                         DN
    PROSITE; PS50050; TNFR_NGFR_2; 4.
                                                                                         RP SEQUENCE FROM N.A.
KW
    RECEPTOR: TRANSMEMBRANE: GLYCOPROTEIN: REPEAT: SIGNAL:
                                                                                         RC TISSUE-SPLEEN:
KW
    PHOSPHORYLATION.
                                                                                         ВX
                                                                                              MEDLINE: 92039815.
FT SIGNAL
                                                                                              ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
    CHAIN
                23 461
                             TUMOR NECROSIS FACTOR RECEPTOR 2.
                                                                                              IMMUNOGENETICS 34:338-340(1991).
                23 257
258 287
288 461
                              EXTRACELLULAR (POTENTIAL).
FΤ
    DOMAIN
                                                                                         RN
    TRANSMEM 258
FT
                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                         PP
                                                                                              SEQUENCE FROM N.A.
ΡŦ
    DOMAIN
                                                                                         RX MEDLINE; 94245292.
                              4 X TNFR-CYS.
PT
    DOMAIN
                39
                      201
                                                                                         RA
                                                                                              BEBO B.F., LINTHICUM D.S.;
ΡT
    REPEAT
                39
                       76
                              TNFR-CYS 1.
                                                                                         RL
                                                                                              IMMUNOGENETICS 39:450-451(1994).
                     118
FT
    REPEAT
                 77
                               TNFR-CYS 2.
                                                                                         RN
                              TNFR-CYS 3.
PΤ
    REPEAT
              119
                     162
                                                                                         RP SECUENCE FROM N.A.
FT
    REPEAT
                163
                      201
                              TNFR-CYS 4.
                                                                                         RX MEDLINE: 93156721.
    DISULFID
                40
                       53
                               BY SIMILARITY.
                                                                                              ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
                              BY SIMILARITY.
FT
    DISULPID
                 54
                       67
                                                                                              MOL. IMMUNOL. 30:165-175(1993).
PT
    DISULFID
                57
                     75
                             BY SIMILARITY.
                                                                                              -!- FUNCTION: RECEPTOR FOR THE-ALPHA, THE ADAPTOR MOLECULE FADD
    DISULFID
               78
                             BY SIMILARITY.
                                                                                                  RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
                      93
PT
                              BY SIMILARITY.
BY SIMILARITY.
PΤ
    DISULFID
                96
                      110
                                                                                         CC
                                                                                                  AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
             100
                                                                                                  PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
FΨ
    DISHLETD
                      118
                                                                                         CC
    DISULFID
              120
                     126
                              BY SIMILARITY.
                                                                                                  SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
                    143
                             BY SIMILARITY.
ΡŦ
    DISULFID
              134
137
                                                                                                  PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
    DISULFID
                      161
                               BY SIMILARITY.
                                                                                              -!- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THERI LEADS TO
PΤ
                             BY SIMILARITY.
             164 179
    DISULFID
                                                                                                  HOMOTRIMERIZATION, ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PΨ
FT CARBOHYD
             171 171
                              POTENTIAL.
                                                                                                  PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
              193
                              POTENTIAL.
                                                                                                  WITH THE DEATH DOMAIN OF TRADD, VARIOUS TRADD-INTERACTING
FT
    CARBOHYD
                     193
                                                                                         CC
    CONFLICT
                141
                      141
                               R -> P (IN REF. 4).
                                                                                         CC
                                                                                                  PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
              196
                             R -> M (IN REF. 1 AND 3).
                                                                                                  TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
    CONFLICT
                     196
                                                                                                  ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
PT CONFLICT
              363 363
                              A -> T (IN REF. 4).
                                                                                         CC
SO SEQUENCE 461 AA: 48316 MW: 0F5D0C44 CRC32:
                                                                                         CC
                                                                                                NF-KAPPA B SIGNALING (BY SIMILARITY).
                                                                                         CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN,
                                                                                         CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                        5.8%; Score 158; DB 1; Length 461;
 Best Local Similarity 27.9%; Pred. No. 3.51e-10;
Matches 29; Conservative 23; Mismatches 48; Indels 4; Gaps 3;
                                                                                         DR EMBL; M60468; G199826; -.
                                                                                              EMBL; M59377; G202097; -.
                                                                                         DR
                                                                                         DR EMBL; X59238; G53579; -
      75 CDSCEDST-YTOLWNWVPECLSCGSRCSSDOVETOACTREONRICTCRPGWYCALSKOEG 133
                                                                                         DR EMBL: X57796; G54849; -.
         ione d'itablication calle et
                                                                                         DR EMBL; L26349; G430733; -.
      96 CNPCTEGVDYTIASNNLPSCLLC-TVCKSGOTNKSSCTTTRDTVCOCEKGSFODKNSPEM 154
                                                                                         DR
                                                                                              EMBL; M76656; G202102; -
                                                                                         DR EMBL; M88067; G202102; JOINED.
                                                                                         DR EMBL; M76655; G202102; JOINED.
     134 CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTD 177
                                                                                         DR PIR; A38634; GQMST1.
        155 CRTCRT--GCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAE 196
                                                                                         DR
                                                                                              PIR: S16677: S16677.
                                                                                         DR PIR; S19021; S19021.
                                                                                         DR HSSP; P19438; 1TNR.
RESULT 15
                                                                                              MGD; MGI:98781; TNFR1.
ID TNR1_MOUSE
                              PRT: 454 AA.
                                                                                         DR PROSITE; PS00652; TNFR_NGFR_1; 3.
                STANDARD:
AC P25118;
                                                                                         DR PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                         DR PROSITE; PS50017; DEATH_DOMAIN; 1.
    01-MAY-1992 (REL. 22, CREATED)
                                                                                         KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
    01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                         FT SIGNAL 1 21 POTENTIAL.
                                                                                                                         TUMOR NECROSIS FACTOR RECEPTOR 1.
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                         PT CHAIN
```

```
FT DOMAIN
                22
                      212
                               EXTRACELLULAR (POTENTIAL).
ΡŦ
    TRANSMEM
               213
                      235
                               POTENTIAL.
FT
    DOMAIN
                236
                      454
                               CYTOPLASMIC (POTENTIAL).
    DOMAIN
                43
                      196
                                4 X TNFR-CYS.
    REPEAT
                 43
                       82
                               TNFR-CYS 1.
FT
    REPEAT
                83
                      125
                               TNFR-CYS 2.
    REPEAT
FT
               126
                      166
                               TNFR-CYS 3.
                167
FΤ
    REPEAT
                      196
                               TNFR-CYS 4.
FT
    DOMAIN
               356
                      441
                               DEATH DOMAIN.
    DISULFID
FΤ
               44
                       58
                               BY SIMILARITY.
    DISULFID
               59
                               BY SIMILARITY.
    DISULFID
FΤ
               62
                       81
                               BY SIMILARITY.
FT
    DISULFID
                84
                       99
                               BY SIMILARITY.
    DISULFID
               102
                      117
FΤ
                               BY SIMILARITY.
ΡT
    DISULFID
               105
                      125
                               BY SIMILARITY.
FΤ
    DISULFID
               127
                      143
                               BY SIMILARITY.
ΡĨ
    DISULFID
               146
                      158
                               BY SIMILARITY.
ΡĨ
    DISULFID
               149
                      166
                               BY SIMILARITY.
FT
    DISULFID
               168
                      179
                               BY SIMILARITY.
    DISULFID
               182
                               BY SIMILARITY.
FΤ
                      191
ΡŦ
    DISULFID
               185
                      195
                               BY SIMILARITY.
    CARBOHYD
               54
                       54
                               POTENTIAL.
    CARBOHYD
               151
                      151
                                POTENTIAL.
    CARBOHYD
               202
                      202
                               POTENTIAL.
    CONFLICT
               394 394
                               R -> G (IN REF. 6).
ΡŦ
SQ SEQUENCE 454 AA; 50129 MW; 4B6EEC09 CRC32;
                        5.7%; Score 156; DB 1; Length 454;
 Best Local Similarity 30.8%; Pred. No. 7.85e-10;
 Matches 32; Conservative 17; Mismatches 44; Indels 11; Gaps 11;
```

- 71 DCPSPG-R-D-T-VCRECEKGT-FTASQNYLRQCLSCKTCRKEMSQVEISPCQADKDTVC 125
- Qy
- 126 GCKENOFORYLSETHFOCVDC-SPCFNGTVTIP-CKETONTVCN 167
- 140 OCEKGSFOD-KNSPEM-CRTCRTGCPRGMVKVSNCTPRSDIKCK 181

Search completed: Thu May 14 16:47:55 1998 Job time : 22 secs.

• 4,



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri May 15 18:56:00 1998; MasPar time 262.16 Seconds 916.449 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-2 Description: (1-2082) from US08918874.seq Perfect Score: 2082

N.A. Sequence: 1 CCAACTGCACCTCGGTTCTA......CATTTTATATTGCTTTACTA 2082 Comp: GGTTGACGTGGAGCCAAGAT.....GTAAAATATAACGAAATGAT

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28

29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.752: Variance 5.463: scale 1.785

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHWWARTES

Re	sult No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
c	1	85	4.1	335		061099	Human brain Expressed	4.21e-39
c	2	85	4.1	22481		T11658	PEDF full length sequ	4.21e-39
Ť	3	83	4.0	2477		T38689	Human CRTAM.	1.01e-37
¢	4	83	4.0	2562	28	T59650	Human dsRNA-dependent	1.01e-37
С	5	83	4.0	2562	15	T03903	Human p68 kinase mRNA	1.01e-37
С	6 7	84	4.0	3234	15	Q92781	Human thymopoietin ge	2.07e-38
		81	3.9	1047	2	Q10572	Human Natriuretic Pep	2.42e-36
С	8	82	3.9	1047	2	Q10572	Human Natriuretic Pep	4.96e-37
	9	81	3.9	1618	7	Q46958	Human cytokine synthe	2.42e-36
	10	81	3.9	1618	2	Q10207	pH15C insert containi	2.42e-36
	11	82	3.9	17327	7	Q44278	Serglycin - proteogly	4.96e-37
	12	80	3.8	429	8	Q60835	Human brain Expressed	1.18e-35
	13	79	3.8	1830		T03731	TNF-R p75IC-binding p	5.73e-35
	14	79	3.8	8342		Q75209	ALL-1 (acute lymphocy	5.73e-35
	15	79	3.8	8391	19	T16333	MLL gene 8.3 kb fragm	5.73e-35

	16	79	3.8	8392	053478	MLL gene 8.3 kb BamHI	5.73e-35
	17	79	3.8	24025 2	T17515	Mutated BRCAl genomic	5.73e-35
	18	79	3.8	24025 2	1 717455	Mutated BRCA1 genomic	5.73e-35
	19	79	3.8	24026 23	1 717527	Mutated BRCA1 genomic	5.73e-35
	20	79	3.8	24026 23	1 117517	Mutated BRCA1 genomic	5.73e-35
	21	79	3.8	24026 2	1 T17526	Mutated BRCA1 genomic	5.73e-35
	22	79	3.8	24 0 26 2	1 117522	Mutated BRCA1 genomic	5.73e-35
	23	79	3.8	24026 2	1 T17516	Mutated BRCAl genomic	5.73e-35
	24	79	3.8	24026 2	1 T17523	Mutated BRCAl genomic	5.73e-35
	25	79	3.8	24026 2	1 T17514	Mutated BRCAl genomic	5.73e-35
	26	79	3.8	24026 2	1 T17521	Mutated BRCAl genomic	5.73e-35
	27	79	3.8	24026 2	1 T17524	Mutated BRCA1 genomic	5.73e-35
	28	79	3.8	24026 2	1 117528	Mutated BRCA1 genomic	5.73e-35
	29	79	3.8	24026 2	1 117530	BRCA1 genomic sequenc	5.73e-35
	30	79	3.8	24026 2	1 T17513	Mutated BRCAl genomic	5.73e-35
	31	79	3.8	24026 2	3 T32612	BRCA1, human breast a	5.73e-35
	32	79	3.8	24026 2	1 T17519	Mutated BRCAl genomic	5.73e-35
	33	79	3.8	24026 1	8 T18325	BRCA1, human breast a	5.73e-35
	34	79	3.8	24026 2	1 T17529	Mutated BRCAl genomic	5.73e-35
	35	79	3.8	24026 2	1 117518	Mutated BRCA1 genomic	5.73e-35
	36	79	3.8	24026 2	1 117512	Mutated BRCA1 genomic	5.73e-35
	37	79	3.8	24029 2	1 717520	Mutated BRCAl genomic	5.73e-35
	38	79	3.8	24031 2	1 T17525	Mutated BRCA1 genomic	5.73e-35
C	39	80	3.8	30967 2	3 T32454	Calpain large subunit	1.18e-35
	40	78	3.7	1926 3	3 T73340	Human GADII cDNA.	2.77e-34
	41	77	3.7	6210 1	1 Q63815	c-fos gene.	1.34e-33
	42	78	3.7	11298 3	3 T86756	Human high affinity I	2.77e-34
	43	78	3.7	11357	9 Q51024	Human FcERI beta chai	2.77e-34
	44	78	3.7	30967 2	3 T32454	Calpain large subunit	2.77e-34
C	45	78	3.7	53577 2	8 T18551	Human polycystic kidn	2.77e-34

ALIGNMENTS

AC	Q61099;
DT	16-MAR-1994 (first entry)
DE	Human brain Expressed Sequence Tag EST01693.
KW	Gene transcription product; genetic markers; tagging; in vivo;
KW	transcription; mapping; locations; chromosomes; chromosomal; ss.
OS	Homo sapiens.
PN	W09316178-A.
PD	19-AUG-1993.
PF	12-FEB-1993; U01294.
PR	12-FEB-1992; US-837195.

ID 061099 standard: DNA: 335 BP.

PESILT 1

(USSH) US DEPT HEALTH & HUMAN SERVICE.

Adams MD, Moreno RF, Venter CJ.

WPI; 93-272882/34.

Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging

of most human genes

Example 4; Page 438; 500pp; English.

The Expressed Sequence Tag was isolated from a human brain cDNA

library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate

tagging of most human genes, for mapping locations of expressed genes

on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue

type, and for prepn. of antisense sequences, probes and constructs. EST01693 has a "Poor" coding probability as evaluated using the

coding-region prediction program CRM. See also Q59041-Q61440.

Sequence 335 BP; 77 A; 94 C; 82 G:

4.1%; Score 85; DB 8; Length 335; Best Local Similarity 80.7%; Pred. No. 4.21e-39; 0; Mismatches 26; Indels 0; Gaps 0; Matches 109: Conservative

151 tttttntnattttttgtagagacgggtttcaccctgttgcccaggctggtctcaaactc 210 1716 TTTTTTTTTTAAATTGAGATGGAGTTTCACTGTGTTGATGAGGCTGGTCTCAAACTC 1657

211 ctgagctcaagcaatctgcccacctaagcctctcaaagtgctggcattacaggcatgagc 270

OS Homo sapiens.

Kev

Location/Oualifiers

FH

DN

```
1656 CCGAGCTCAAGCAATCCACCTGCCTCAGCCTATCAAAGTGCTGGGATTACAGGCATGAGC 1597
     271 caccgtgcctggcct 285
    ||||| ||||||
1596 CACCGCATGTGGCCT 1582
RESULT
        2
ID T11658 standard; DNA; 22481 BP.
   T11658:
    16-JAN-1997 (first entry)
    PEDF full length sequence and flanking sequences.
    Pigment epithelium-derived factor: PEDF: neuronal cells: neurons:
    qlial cells; qliastatic; qliosis; central nervous system; CNS;
    neurodegenerative disease; injury; neuronotrophic; brain cells;
    Parkinson's disease; photoreceptor cells; retina; inhibition;
    proliferation; immunoassay; antibody; ageing; degenerative disease;
OS
    Homo sapiens.
PN
    W09533480-A1.
    14 - DRC - 1995
    06-JUN-1995: U07201.
    07-JUN-1994: US-257963.
    30-DEC-1994; US-367841.
    (USSE ) US DEPT HEALTH & HUMAN SERVICES.
    Becerra SP, Chader GJ, Schwartz JP, Taniwaki T;
    WPI: 96-039966/04.
    P-PSDB: R90287.
    Use of pigment epithelium derived factor - for enhancing neuronal
    cell survival and inhibiting glial cell proliferation, useful, e.g.
    in CNS cell culture or to treat neuro-degenerative diseases
    Disclosure; Page 100-122; 151pp; English.
    Pigment epithelium-derived factor (PEDF) has both neuronotrophic and
    gliastatic activity, making it useful in cases where neurons die
    quickly and glia tend to proliferate (gliosis), e.g. in CNS cell
    culture, in neurodegenerative diseases and in CNS injury. The
    neuronotrophic effect of PEDF is especially useful for enhancing
    survival of neuronal cell cultures intended for use in
    transplantation. These include cultures of human foetal brain cells
    and neural retina and photoreceptor cells . The gliastatic activity
    of PEDF can be applied to inhibiting glial cell proliferation in
    certain tumours. Antibodies directed against PEDF can be used for
    inhibiting PEDF activity or in an immunoassay for determining
    levels of PEDF in fluid, cellular or tissue samples e.g for
    determining ageing and/or other degenerative diseases.
  Sequence 22481 BP; 5280 A; 5708 C; 6136 G;
                        4.1%; Score 85; DB 24; Length 22481;
 Best Local Similarity 82.0%; Pred. No. 4.21e-39;
 Matches 109: Conservative 0: Mismatches 24: Indels 0: Gaps 0:
  15305 tttttgtatttttagtagagacggggtttcaccatgttgcctaggctggtctcaaactcc 15364
         1715 TTTTTTCTTTTTAAATTGAGATGGAGTTTCACTGTGTTGATGAGGCTGGTCTCAAACTCC 1656
Db 15365 cqqqctcaaqcqatccacccqccttqqcctcccaaaqtqctqqqattacaqqcqtqaqcc 15424
    1655 CGAGCTCAAGCAATCCACCTGCCTCAGCCTATCAAAGTGCTGGGATTACAGGCATGAGCC 1596
Db 15425 accgcgcctggcc 15437
         mir iin
   1595 ACCGCATGTGGCC 1583
RESULT 3
ID T38689 standard; cDNA; 2477 BP.
  T38689:
    12-JAN-1997 (first entry)
    Human CRTAM.
KW Cytotoxic or regulatory T-cell associated molecule; CRTAM;
KW physiology; cell regulation; development; differentiation;
KW T-cell; progenitor; ss.
```

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ΡŢ
    CDS
                    38...1219
FT
    /*tag= a
    W09634102-A1.
PN
PD
     31-OCT-1996.
     25-APR-1996: U05329.
     26-APR-1995; US-429742.
     (SCHE ) SCHERING CORP.
PA
ΡI
     Bazan JF, Kennedy JL, 2lotnik A;
DR
    WPI: 96-497634/49.
DR
    P-PSDB: W04404.
    Cytotoxic or Regulatory T-cell associated Mol., CRTAM, - useful to
    develop prods, for diagnosis and treatment of conditions involving
    abnormal cell physiology
    Claim 3; Page 60-62; 74pp; English.
     CRTAM proteins are involved in the regulation of celluar physiology,
CC
     development, differentiation or function of various cell types,
CC
     including haematopoietic cells and partic. T-cell progenitors. The
     prods. can be used to develop prods. for the diagnosis and treatment
     of conditions associated with abnormal physiology or development,
     including abnormal proliferation, e.g. cancers, or degenerative
    conditions. The physiology or development of a cell can be modulated
    by contacting the cell with an agonist or antagonist (i.e. an anti-
CC CRTAM peptide antibody) of a CRTAM peptide.
SO Seguence 2477 BP: 798 A: 527 C: 548 G:
                        4.0%; Score 83; DB 24; Length 2477;
  Best Local Similarity 81.2%; Pred. No. 1.01e-37;
  Matches 108; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
   1673 ggccaggcgcggtggctcatgcctgtaatcctagcactttgggaggctgaggtaggcaga 1732
          iim" iriniimmimimm rimmi"iliniili lii-li
     1583 GOCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGA 1642
   1733 tcacttgaggtcaggagttggagaccagcctggccaacatagtgaaaccccgtctctact 1792
          1643 TECCTEGACCECCGCACTETCACACCACCCTCATCAACACACTCAAACTCCATCTCAATT 1702
   1793 aaaaatgcaaaaa 1805
          -100 î 1000
   1703 TAAAAAGAAAAA 1715
RESULT 4
ID T59650 standard; cDNA; 2562 BP.
AC
    T59650:
     04-MAY-1997 (first entry)
     Human dsRNA-dependent protein kinase cDNA.
     dsRNA-dependent protein kinase; PKR; 2-5A synthetase;
KW
     2-5A-dependent RNase; RNase L; 2-5A system; antiviral;
     RNA degradation; transgenic plant; tobacco; disease resistance;
KW crop protection; tobacco mosaic virus; tobacco etch virus;
KW
    alfalfa mosaic virus: vector pAM2200; ss.
0S
     Homo sapiens.
PH
    Key
                    Location/Oualifiers
FT
    CDS
                    187...1842
FT
     /*tag= a
     WO9639806-Al.
     19-DEC-1996
    07-JUN-1996; U09895.
PF
PR
    07-JUN-1995; US-487797
     (CLEV-) CLEVELAND CLINIC FOUND.
PΑ
    Mitra A, Silverman RH;
מח
    WPI: 97-051617/05.
DR
    P-PSDB: W12705.
    Transgenic plants co-expressing 2-5A-dependent RNase and 2-5A
     synthetase - have increased resistance to viral infection esp. to
     tobacco mosaic virus, tobacco etch virus or alfalfa mosaic virus
    Disclosure; Page 145-146; 189pp; English.
    A cDNA clone (T59650) codes for human dsRNA-dependent protein
    kinase (PKR) (W12705), an antiviral protein that is believed to
    phosphorylate the alpha subunit of translation factor eIF2-alpha,
```

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CC which indirectly inhibits protein synthesis initiation. Novel
                                                                                    DT 09-DEC-1995 (first entry)
    transgenic plants, such as transgenic tobacco, express (together or
    alone) the PKR, human 2-5A synthetase (see also T59645) and human
    or mouse 2-5A-dependent RNase (see also T59648-49). When the
    plants are exposed to tobacco mosaic virus, tobacco etch virus and
    alfalfa mosaic virus, necrotic local lesions occur instead of
                                                                                    77
    typical systemic infections.
                                                                                    FT
    Sequence 2562 BP; 842 A; 478 C; 501 G; 741 T;
                      4.0%; Score 83; DB 28; Length 2562;
  Best Local Similarity 83.2%; Pred. No. 1.01e-37;
  Matches 104; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
    2223 tttttgtgtttttaataaagacagggtttcaccatgttggccaggctggtctcaaactcc 2282
    2283 tgacctcaagtaatccacctgcctcggcctcccaaagtgctgggattacagggatgagcc 2342
          1655 CGAGCTCAAGCAATCCACCTGCCTCAGCCTATCAAAGTGCTGGGATTACAGGCATGAGCC 1596
    2343 accqc 2347
    1595 ACCGC 1591
RESULT 5
    T03903 standard; DNA; 2562 BP.
    T03903:
    27-JAN-1996 (first entry)
    Human p68 kinase mRNA (PKR) coding sequence.
    PK68; p68 kinase; mrPk68; ss.
os
    Homo sapiens.
    WO9522245-A.
PΠ
    24-AUG-1995.
    16-PEB-1995: D02058.
    18-FEB-1994: US-198973.
DD
    (CLEV-) CLEVELAND CLINIC FOUND.
    Sengupta DN, Silverman RH;
DΒ
    New transgenic plants resistant to viral infection contg. 2-5A-dependent
PΤ
    RNase - useful in developing products useful in gene therapy against
    viral disease and cancer.
    Claim 4; Figure 18; 196pp; English.
    PKR (PK68) is a lysine - arginine mutant PKR (mrPK68). The mutant
    PKR protein binds to dsRNA but has no kinase activity. A transgenic
    plant is claimed which includes the nts in T03903 or any part of
    this sequence which contains the complete or partial coding
    sequence for PKR or the ds RNA binding domain of PKR. The
    translation product of the complete coding sequence for human
    p68 kinase mRNA (PKR) is given in R82663.
    Sequence 2562 BP: 842 A: 479 C: 501 G: 740 T:
                       4.0%; Score 83; DB 15; Length 2562;
  Best Local Similarity 83.2%; Pred. No. 1.01e-37;
  Matches 104; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
    2223 tttttgtgtttttaataaagacagggtttcaccatgttggccaggctggtctcaaactcc 2282
    2283 tgacctcaagtaatccacctgcctcggcctcccaaagtgctgggattacagggatgagcc 2342
    1655 CGAGCTCAAGCAATCCACCTGCCTCAGCCTATCAAAGTGCTGGGATTACAGGCATGAGCC 1596
    2343 accgc 2347
    1595 ACCGC 1591
                                                                                    FT
RESULT 6
ID 092781 standard; DNA; 3234 BP.
AC 092781:
```

```
Human thymopoietin gene fragment.
DE
K₩
    Thymopoietin; diagnostic; therapeutic; gene therapy; ss.
0S
    Homo sapiens.
                    Location/Oualifiers
FH
                    1...54
    eyon
    /*tag= a
    /note= "3' end of exon 6"
                    1357..1445
    exon
FΤ
    /*tag= b
ΡT
    /note= "exon 7"
FΤ
                    2572..3234
    exon
ΡŢ
    /*tag= c
FT
     /note= "exon 8 - partial sequence"
PN
     W09517205-A1.
    29-JUN-1995
PΩ
    13-DEC-1994: U14356.
PF
PR
     21-DEC-1993: US-171382.
     (IMMU-) IMMUNOBIOLOGY RES INST INC.
PΔ
     Culler MD, Goldstein G, Harris CA, Setcavage DR;
     Shenbagamurthi P, Siekierka JJ, Talle MA:
    WPI: 95-240474/31.
    Polynucleotide(s) encoding human thymopoietin proteins - used to
     develop prods, for diagnosis and therapy involving immune or nervous
ΡĪ
     system conditions.
    Disclosure; Fig 11a-11c; 85pp; English.
PS
    The sequence represents a fragment of the human thymopoletin gene,
     including the 3' end of exon 6, exon 7 and a partial sequennce for
     exon 8. DNA encoding human thymopoletin, isolated from
    a cDNA library prepared from human thymus RNA, may be expressed in
    a host cell e.g. bacterium (preferably Escherichia coli), fungus,
     insect or mammalian cell for production of recombinant thymopoietin.
     Thymopoietin has a regulatory effect on the mammalian immune system,
    and can be used for treating/modulating an immune or nervous system
    condition, and for the treatment of chronic infection, autoimmune
    disorders and certain affective psychiatric or neurological
    disorders. The protein and the DNA can be used as diagnostics;
     the DNA can be used in gene therapy.
SQ Sequence 3234 BP; 933 A; 577 C;
                                             617 G;
                        4.0%; Score 84; DB 15; Length 3234;
  Best Local Similarity 80.9%; Pred. No. 2.07e-38;
  Matches 110; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
      898 tttttgtatttttagtagagatgggatttcactatgttggtcaggctggtctcgaactcc 957
    1715 TTTTTCTTTTAAATTGAGATGGAGTTTCACTGTGATGAGGCTGGTCTCAAACTCC 1656
      958 tgacctcaggtgatccacccgcctcagcctcccaaagtgctgggattacaggcgtgagcc 1017
    1655 CGAGCTCAAGCAATCCACCTGCCTCAGCCTATCAAAGTGCTGGGATTACAGGCATGAGCC 1596
     1018 accqtacccqqcccaa 1033
         THÍ I THE R
    1595 ACCGCATGTGGCCTAA 1580
TD
    Q10572 standard; DNA; 1047 BP.
    010572;
    09-APR-1991 (first entry)
    Human Natriuretic Peptide Receptor B.
DR
KW
     NPRB: ANP: BNP: CNP: kidney failure: heart failure; protein kinase;
KW
    hyperaldosteronism; qlaucoma; quanyl cyclase.
     Homo sapiens.
FH
    Key
                    Location/Qualifiers
FΤ
    Peptide
                    1..22
PΤ
    /label= signal sequence
    Protein
FT
                    12
     /label= mature NPBR
FT
    Domain
                    23..455
FT /label= extracellular domain
   /note= "binds natriuretic peptides A,B and C]"
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PT Domain
                                 456..456
        /label= transmembrane domain
PT Domain 479..1047
FT /label= cytoplasmic domain
        /note= "GC and protien kinase activity"
        Modified -site 24..26
     /label= N-glycos_site
FT Modified -site 35..37
FT /label= N-qlvcos_site
FT
        Modified -site 161..163
FT /label= N-glycos_site
     Modified -site 195..197
       /label= N-glycos site
FT
       Modified -site 244..246
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        Modified -site 277..279
PΨ
       /label= N-glycos_site
PΤ
        Modified -site 349..351
PT
FT /label= N-glycos site
        Modified -site 600..602
        /label= N-glycos site
        W09100292-A.
DN
PD 10-JAN-1991.
       22-JUN-1990; U03586.
23-JUN-1989: US-370673.
pp
PR
        (GETH ) GENENTECH INC.
PA
        Chang M, Goeddel D, Lowe D;
        WPI; 91-036711/05.
        N-PSDB; Q10324.
        Natriuretic protein receptor B - for diagnosis and treatment of
PΤ
        kidney failure, heart failure, hyperaldosteronism, glaucoma etc.
PΤ
PS
        Claim 3; Fig 1; 49pp; English.
CC
        The sequence was derived from the DNA encoding natriuretic peptide
       receptor B, NPRB, having guanyl cyclase (GC) activity and protein
        kinase activity. The DNA can be inserted into expression vectors
        for the prodn. of the protein, opt. after being mutated to produce
        NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=
CC 114,952). The protein (or variants) can be used in treatment of
        natriuretic peptide disorders, and also to isolate peptides using
CC
        affinity chromatography. Antibodies with affinity for NPRB can
       also be prepd.
       Sequence 1047 BP: 87 A: 15 C: 83 G: 51 T:
                                          3.9%; Score 81; DB 2; Length 1047;
  Query Match: 5.39; Score of; DB 2; Dength 1047;
Best Local Similarity 9.1%; Pred. No. 2.42e-36;
Matches 90; Conservative 279; Mismatches 613; Indels 12; Gaps 11;
           29 vvnnnhnnsyawawnrvqnavanavnanqrannvdnrnvssnnngacsnynannsavdnk 88
         :: : : | |: :: | : : : : : | : : | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
           89 nyhdndnnngngcvynaasvarnashwrnnnntagavasgnsakndhyrtnvrtgnsank 148
          ٥v
          149 ngnnyytn--hghnnwtaraannyndartddrnhyntnngynnanngsnnsynhnyyarn 206
         Q٧
          207 nggnnnathnnrangrnvync-gnnnmnhnnnnnanrnnntngdyvnnyndvngnsnrag 265
          Qy
          266 n-tratgrnwndnrtrnnananrn-ann-tvnvntyrnnnnnnynnnnnrnnnrarndng 322
         |: :: :| | |: | :: | : : : : | 401 AGTGTCCAGCAGGAGTCTCATAGATCAGAATATACTGGAGCCTGTAACCCGTGCACAGAGG 460
          323 vnngnsnmnnnagenydgnnny-anvnnntnnnggtrndgnrnvnkmngrryhgvtgnvv 381
         382 mdknndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgannsdnnncan 441
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521 AATCAGGTCAAACAATAAAAGTTCCTGTACCACGACCA-GAGACACCGTGTGTCAGTGT 579
    442 dnddnscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmnwrnrwnnnnn 501
    Qy
    502 gnsnryhkgagsrntnsnrgssygsnmtahgkynnnantghnkgnvvankhvnkkrnnnt 561
       639 GTGTCCCAGAGGGATGGTCAAGGTCAGTAATTGTACGCCCCGGAGTGACATCAAGTGCAA 698
    562 rnynnnnkhmrdvnnnhntrnngaendnnnnenvtnyenrgsnndnnnndsnnndwmnry 621
    0ν
    622 snnn-dnykgmannhnsnnsshgsnkssncyvdsrnynkntdygnasnrstannddnnan 680
    681 yakknntannnnsgnnnnttgmnaadvysngnnnnnnanrsgnnynngndnsnknnvnkv 740
    0v
    741 rngnrnynrnsndrtnnnnnnynnmnrcwandnanrndngnnkgnnrrnnknggtsnndn 800
    801 nnnrmnnvannnnknvnnrtnavnnnkrkanannynnnnhsvannnkrqntvnanandsv 860
    938 GGCGTTCATGTCCTTCACGAGTTCCTGGGGCGGAGGACAATGCCCGCAACGAGACCCTGA 997
Qy
    861 tnynsdnygntansanstnmnyvtnnndnytchdanndnndvykvntngdaymvvsgnng 920
    921 rngnrhannnarmananndayssnrnrhrnhdnnrnrngyhtgnycagyygnkmnrycnn 980
   981 gdtvntasrmnsngnanknhyssttkdandnngc 1014
        la a famanlaft
  1117 GCAGAAGCTGAAGGGTGTCAGAGGAGGAGGCTGC 1150
PECULT.
ID 010572 standard; DNA; 1047 BP.
AC 010572:
   09-APR-1991 (first entry)
DT
DE Human Natriuretic Peptide Receptor B.
KW NPRB; AMP; BMP; CMP; kidney failure; heart failure; protein kinase;
   hyperaldosteronism; glaucoma; guanyl cyclase.
OS
   Homo sapiens.
               Location/Oualifiers
PH Key
FT Peptide
              1...22
   /label= signal sequence
   Protein 12
27
FT /label= mature NPBR
   Domain
               23 455
   /label= extracellular domain
   /note= "binds natriuretic peptides A,B and C]"
   Domain 456..456
PΤ
FT /label= transmembrane domain
FT
   Domain 479..1047
PT /label= cytoplasmic domain
PT /note= "GC and protien kinase activity"
   Modified -site 24..26
FT
PT /label= N-qlycos_site
FT Modified -site 35..37
FT /label= N-glycos_site
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FT /label= N-glycos_site
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   Modified site 600.602
   /label= N-glycos site
   WO9100292-A.
   10-JAN-1991.
   22-JUN-1990; U03586.
   23-JUN-1989: US-370673
   (GETH ) GENENTECH INC.
   Chang M. Goeddel D. Lowe D:
   WPI: 91-036711/05.
   N-PSDB: 010324.
   Natriuretic protein receptor B - for diagnosis and treatment of
   kidney failure, heart failure, hyperaldosteronism, glaucoma etc.
   Claim 3; Fig 1; 49pp; English.
   The sequence was derived from the DNA encoding natriuretic peptide
   receptor B, NPRB, having guanyl cyclase (GC) activity and protein
   kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce
   NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=
   114,952). The protein (or variants) can be used in treatment of
   natriuretic peptide disorders, and also to isolate peptides using
   affinity chromatography. Antibodies with affinity for NPRB can
   also be prepd.
SQ Sequence 1047 BP; 87 A; 15 C; 83 G; 51 T;
                   3.9%; Score 82; DB 2; Length 1047;
 Best Local Similarity 9.8%; Pred. No. 4.96e-37;
 Matches 100; Conservative 287; Mismatches 618; Indels 15; Gaps 15;
     17 vrnngarnntnavvnnnhnnsyawawnrvgnavanavnangrannvdnrnvssnnngacs 76
   77 nynannsavdnknyhdndnnngngcvynaasvarnashwrnnnntagavasgnsa-kndh 135
   136 yrtnyrtgnsankngnnyvtnhghnnwtaraannyndartddrnhyntnngynnanngsn 195
   196 nsvnhnvyarnnggnnnathnnrangrnvyncgnnmnhnnnnnanrnnntngdyvnnyn 255
   ::::|: |: |: |: || :::|| :: ::
1018 TGGGCTGCAAGTATCTGTTACTCAGGGTCT-CGTTGCGGGGCATTGTCCTCCGCCCCAGGA 960
    256 dvnqnsnragntratgrnwndnrtrnnananrnanntvnvntyrnnnnnnynnnnnrnnn 315
    316 rarndngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrryhg 375
    CD
    376 vtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgannsd 435
    436 nnncandnddnscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmnwrnr 495
    496 wnnnnngnsnryhkgagsrntnsnrgs-sygsnmtahgkynnnantghnkgnvvankhvn 554
    555 kkrnnntrnvnnnnkhmrdvnnnhntrnnga-endnnnnenvtnyenrgsnndnnnndsn 613
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614 nndwmnrysnnndnykgmannhnsnnsshgsnkssncyydsrnynkntdygnasnrstan 673
        Tim i tari i tri t | mar t iii t | m
     604 TTTTATCCTGGAAGCTTCCTTTTTCACACTGACACGGTGTCTCTGGTCGTGGTAC-AG 546
     674 nddnnanyakknntannnnsgnnnnttgmnaadvy-sngnnnnnnanrsgnnynngndns 732
     733 nknnvnkvrngnrnynrnsndrtnnnnnnvnnmnrcwandnanrndngnnkgnnrrnnkn 792
     793 ggtsnndnnnnrmnnyannnnknvnnrtnaynnnkrkanannynnnnhsvannnkrgntv 852
     Dh
     853 nanandsytnynsdnygntansanstnmnyytnnndnytchdanndnndyykyntngday 912
     913 myvsgnngrngnrhannnarmananndavssnrnrhrnhdnnrnrngvhtgnvcagvvgn 972
     Db
     973 kmnrvcnngdtyntasrmnsngnanknhyssttkdandnngcnnnnnrgdynmkgkgkmr 1032
        and the mark mandata it is a close
     248 CATGGTCTGGTTCCCGACGCTGTCCTGGCTCCTGGATAGCGCCCTGCTCGAGCGCTCGAG 189
RESULT 9
ID 046958 standard; cDNA; 1618 BP.
AC 046958;
    25-JAN-1994 (first entry)
    Human cytokine synthesis inhibitory factor clone pH15C.
    Mammalian cytokine synthesis inhibitory factor; CSIF; interleukin 10;
    IL-10; immune system imbalance; human T cell; Leischmaniasis;
    rheumatoid arthritis; systemic lupus erythematosus; thyroiditis;
    myasthenia gravis; insulin-dependent diabetes mellitus: ss.
OS
    Homo sapiens.
FH
                 Location/Qualifiers
    Key
PT
    CDS
PT 
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    mat_peptide
               85..564
    /*tag= b
    /product= mature CSTF
    US5231012-A.
PD 27-JUL-1993.
PF 28-JUN-1989: 372667.
    28-JUN-1989: US-372667.
    20-DEC-1989: US-453951.
    06-AUG-1990; US-546235.
    20-JUL-1992; US-917806.
    (SCHE ) SCHERING CORP.
    Bond MW, Moore KW, Mosmann TR, Vieira PJM;
    WPI: 93-249726/31.
    P-PSDB; R39714.
    Genes and proteins encoding cytokine synthesis inhibitory factors
    · useful in treating diseases associated with cytokine
    imbalances, e.g. parasitic infections and auto-immune disorders
    Claim 1; Fig 4; 23pp; English.
    A human T cell cDNA library was screened with probes based on the
    murine CSIF gene. Two clones carrying plasmids pH5C and pH15C were
    identified. (These two expression vectors are claimed). The CSIF
    polypeptide they encode inhibits synthesis of cytokines associated
    with delayed type hypersensitivity responses. CSIF (also called IL-
    10) can be used to treat diseases associated with cytokine
    imbalances, such as leichmaniasis and MHC-associated autoimmune
    diseases caused by excessive production of interferon-gamma, e.g.
   rheumatoid arthritis, SLE, IDDM, myasthenia gravis and thyroiditis.
SQ Sequence 1618 BP; 463 A; 367 C; 356 G; 432 T;
```

3.9%; Score 81; DB 7; Length 1618;

Best Local Similarity 79.1%; Pred. No. 2.42e-36;

```
Matches 110; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
   1168 qttctaqqccqqqcqcqqtqqctcacqcctqtaatcccaqcactttqqqaqqctqaqqcq 1227
    1577 GTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCA 1636
    1228 ggtggatcacttgaggtcaggagttcctaaccagcctggtcaacatggtgaaaccccgtc 1287
          iidin midi diida mdoo'doo iidaa a'n
     1637 GGTGGATTGCTTGAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAACTCCATC 1696
    1288 totactaaaaatacaaaaa 1306
    || | | | ||| ||||
1697 TCAATTTAAAAAGAAAAA 1715
RESIDE 10
ID Q10207 standard; cDNA; 1618 BP.
    010207:
    19-MAR-1991 (first entry)
    pH15C insert containing Human cytokine synthesis inhibitory
DE
     factor.
    Delayed-type hypersensitivity; DTH; leishmaniasis; parasite;
    MHC-associated autoimmune disease: interferon-gamma; ds.
KW
OS
    Homo sapiens.
                    Location/Qualifiers
PH
    Key
    CDS
PΨ
     /*tag= a
FT
PN
     EP-405980-A.
     02-JAN-1991.
DΠ
PF
     28-JUN-1990; 307091
     28-JUN-1989: US-372667.
PR
     20-DEC-1989: US-453951.
PR
    (SCHE ) SCHERING CORP.
     Mosmann TR, Moore KW, Bond MW, Vleira PJM:
    WPT: 91-009290/02
DΒ
    R-PSDB: R10158.
     Mammalian cytokine synthesis inhibitory factors - capable of
    inhibiting synthesis of cytokine(s) associated with delayed-type hypersensitivity and useful in treatment of e.g. leishmaniasis
     Disclosure; Fig 4; 31pp; English.
    The gene product may be used in treatment of diseases associated
    with MHC-linked immune response, supressing a cell mediated or
     humoral immune response. It may specifically be used to treat
    delayed-type hyper-sensitivity, leishmaniasis, and immune disorders.
    Sequence 1618 BP: 461 A: 369 C: 356 G: 432 T:
                         3.9%; Score 81; DB 2; Length 1618;
  Best Local Similarity 79.1%; Pred. No. 2.42e-36;
  Matches 110: Conservative 0: Mismatches 29: Indels 0: Gaps 0:
     1168 gttctaggccgggcgcggtggctcacgcctgtaatcccagcactttgggaggctgaggcg 1227
    1577 GTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCA 1636
     1228 qqtqqatcacttqaqqtcaqqaqttcctaaccaqcctqqtcaacatqqtqaaaccccqtc 1287
    1637 GGTGGATTGCTTGAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAACTCCATC 1696
    1288 totactaaaaatacaaaaa 1306
         11 1 1 1111 11111
     1697 TCAATTTAAAAAGAAAAA 1715
ID Q44278 standard; DNA; 17327 BP.
    044278:
    24-NOV-1993 (first entry)
DE Serglycin - proteoglycan peptide core.
    Haematopoietic cell secretory granule proteoglycan;
    positive; negative; transcriptional regulatory element;
    enhancer; eukaryotic promoter; constitutive suppressor;
KW TATA-box: SS.
OS Homo sapiens.
```

```
FH Key
                    Location/Qualifiers
FT
     misc_signal
                    373...621
    /*tag= a
/note= "5' regulatory region;
FΨ
     claim 1-3, page 78"
FT
                    373..433
FT
     misc_signal
     /*tag= b
     /note= "negative transcriptional regulatory element;
FΤ
FT
     claim 6 and 9-10, page 78-79"
PΨ
     enhancer
ΡŦ
     /*tag= c
     /note= "enhancer transcriptional regulatory element;
FT
     claim 11 and 14-15, page 79*
PT
     /*taq= d
     /note= "eukaryotic promoter element;
claim 16 and 19-20, page 80"
FĪ
ΡĪ
ΡĪ
                    675..16646
ΡŦ
     /*tage e
ΡĪ
     /label= serglycin
ΡT
     exon
                     622...753
PT
     /*tag= f
FT
     /number= 1
ΡĪ
     exon
                     9597..9744
     /*tag= g
27
     /number= 2
FT
     eron
                    16397...17327
FΤ
     /*tag= h
     /number= 1
FΤ
     siq_peptide
                    675..9598
    /*tag= i
/note= "interrupted by exon 1"
ΡT
ΡŦ
FT
     misc RNA
                    16449..16502
     /*tag= j
PΨ
PT
     /note= "serine-glycine rich glycosaminoglycan
     attachment region
ΡT
     polyA signal 17062..17067
PT
ΡT
     /*tag= k
FT
     misc difference 6135
     /*tag= 1
PΨ
     /note- "base represented as N in the specification"
     W09313119-A.
DN
PD
     08-JUL-1993.
     23-DEC-1992: U11194.
PF
     03-JAN-1992; US-816289.
PR
     02-JUL-1992; US-906871.
PA
     (BGHM ) BRIGHAM & WOMENS HOSPITAL.
     Avraham S. Stevens RL:
DR
     WPI: 93-227261/28.
DR
     P-PSDB: R39393.
PΤ
     Transcription regulatory elements of ser-glycin gene - specific
     for haematopoietic cells, also trans-acting transcriptional
PΨ
     binding factors
PS
     Disclosure: Fig 4B-J: 112pp: English.
     A negative transcription regulatory element (a constitutive
CC
     suppressor) between residues -250 and -190 (see tag b) of the 5'
     flanking region of the human serglycin gene, a positive
     (hematopoietic cell enhancer) regulatory element located between
     residues -118 and -81 (see tag c), an equiv. of the TATA-box and
     a novel eukarvotic promoter that utilises such equiv. (see tag d)
     are identified. The regulatory elements, vectors and hosts
     provided with these elements, are useful in the control of gene
     transcription of heterologous genes in eukaryotic cells, esp.
     hematopoietic cells.
SO Sequence 17327 BP;
                           4936 A: 3604 C: 3741 G: 5045 T:
                         3.9%; Score 82; DB 7; Length 17327;
  Best Local Similarity 83.1%; Pred. No. 4.96e-37;
  Matches 103; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Db 11013 gccaggtgtggtggtcatgcctgtaatcccagcactttgggaggccgaggcgggggat 11072
          im"ni jirijamimimmimmimmi"nii iii iiiii iii
     1584 GCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGAT 1643
```

FT misc_diffe FT /*tag= c

```
Db 11133 caaa 11136
          111
Ov 1704 AAAA 1707
RESULT 12
ID 060835 standard: DNA: 429 BP.
    060835:
    16-MAR-1994 (first entry)
    Human brain Expressed Sequence Tag EST01613.
    Gene transcription product; genetic markers; tagging; in vivo;
    transcription; mapping; locations; chromosomes; chromosomal; ss.
20
    Homo sapiens.
    W09316178-A.
    19-AUG-1993.
    12-FEB-1993: U01294.
    12-FEB-1992: US-837195.
     (USSH ) US DEPT HEALTH & HUMAN SERVICE.
    Adams MD, Moreno RF, Venter CJ.
    WPI: 93-272882/34
PΤ
    Enriched oligonucleotides and corresp. sequences - used as
    markers for human genes transcribed in-vivo, facilitate tagging
    of most human genes
    Example 4; Page 398; 500pp; English.
    The Expressed Sequence Tag was isolated from a human brain cDNA
    library as part of a large set of ESTs which can be used as markers
     for human genes transcribed in vivo. They can be used to facilitate
    tagging of most human genes, for mapping locations of expressed genes
    on chromosomes, for individual or forensic identification, for mapping
    locations of disease-associated genes, for identification of tissue
    type, and for prepn. of antisense sequences, probes and constructs.
     EST01613 has a "poor" coding probability as evaluated using the
    coding-region prediction program CRM. See also Q59041-Q61440.
    Sequence 429 BP; 140 A; 87 C; 99 G; 100 T;
                        3.8%; Score 80; DB 8; Length 429;
 Best Local Similarity 79.1%; Pred. No. 1.18e-35;
  Matches 106; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
       99 ggccgggtgtggtgnctcatgcctgtaatcccagcactttgggaggctgaggcgggtggn 158
    1583 GGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGA 1642
    159 tcacttgaggtcaggagttcgagaccagcctagccaacatggcgaaaccacatctctact 218
     219 aaaaatacaaaaaa 232
          1111 111111
    1703 TAAAAAGAAAAAA 1716
RESULT 13
ID T03731 standard; cDNA; 1830 BP.
    26-MAR-1996 (first entry)
    TNF-R p75IC-binding protein 75.3 partial cDNA.
    Tumour necrosis factor receptor; TNF-R; p75IC;
    intracellular domain binding protein; human immunodeficiency virus;
    HTV: SS.
    Homo sapiens.
                    Location/Oualifiers
    misc_difference 354
    /note- "base n at position 354 is not identified
     in the specification"
    misc_difference 430
FT /*tag= b
```

```
/note= "base n at position 438 is not identified
     in the specification"
     misc_difference 544
PΨ
     /*tag= d
     /note= "base n at position 544 is not identified
     in the specification"
FŦ
     misc difference 677
PŤ
     /*tag= e
     /note= "base n at position 677 represents an
     undetermined sequence of unknown length"
FΤ
     misc_difference 682
     /*tag= f
     /note= "base n at position 682 is not identified
     in the specification"
FT
     misc_difference 729
FΤ
    /*tag= g
/note= "base n at position 729 is not identified
     in the specification"
FΤ
     variation
    /*tag= h
     /note= "base n at position 743 is not identified
FT
     in the specification'
FT
     misc difference 762
FT /*tag= i
     /note= "base n at position 762 is not identified
     in the specification"
     misc_difference 779
    /*tag= 1
     /note- "base n at position 779 is not identified
FT
FT
     in the specification"
     W09531544-A1.
     23-MOV-1995
חם
     11-MAY-1995: U05854.
     11-MAY-1994; IL-109632.
     02-OCT-1994: IL-111125.
     (WEIN/) WEINWURZEL H.
     (YEDA ) YEDA RES & DEV CO LTD.
     Boldin M. Mett I. Varfolomeev E. Wallach D:
     WPI: 96-010930/01.
     TNF-NGF receptor superfamily intracellular domain-binding proteins -
     useful for modulating receptor function, e.g. for treating tumours
     or HIV-infected cells
     Claim 13; Fig lb; 96pp; English.
     A cDNA clone (T03731) coding for a portion of novel human protein
     75.3 was obtd. from HeLa cDNA by yeast 2-hybrid analysis. 75.3 is
     capable of binding the intracellular domain of tumour necrosis factor
     receptor (TNF-R) protein p75. The cDNA can be used to produce 75.3 (or fusion proteins including 75.3) in transformant host cells for
     use in modulating TNF-R activity as a means of treating tumours or
     e.g. HIV-infected cells.
     Sequence 1830 BP; 604 A;
                                    349 C: 384 G:
                         3.8%: Score 79: DB 17: Length 1830;
  Best Local Similarity 82.1%; Pred. No. 5.73e-35;
  Matches 101; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
       89 ggtggctcatgcctgtaatcccagcaccttgggaggctgaggcaggaggattgcctaagc 148
          tisiimmimimmuusin nii siininiinii ilmir ril
     1593 GGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTTGAGC 1652
      149 ccaggagtttgacatcagcctgggcaacatggtgaaaccccatctctacaaaaaatgcaa 208
     1653 TCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAACTCCATCTCAATTTAAAAAGAAA 1712
          111
     1713 AAA 1715
```

FT /note= "base n at position 430 is not identified

in the specification" misc difference 438

```
RESULT 14
ID 075209 standard; cDNA; 8342 BP.
    075209:
    23-AUG-1995 (first entry)
    ALL-1 (acute lymphocytic leukaemia-1) breakpoint cluster region.
    Acute lymphoblastic leukaemia; acute nonlymphoblastic leukaemia;
    chromosomal translocation; abnormality; detection; rearrangement;
KW
    breakpoint cluster region; Alu repeat; chromosome 11; probe B859; ds.
0S
    Homo sapiens.
PH
                    Location/Oualifiers
     exon
                     1...263
     /*tag= a
     /number= 5
                    264..2352
ΡT
     intron
FT
     /*tag= b
                    593 ... 666
P7
    exon
    /*tag= c
     /number= 6
     intron
                    667..798
PΨ
    /*tag= d
    repeat_unit
                    799..1108
    /*tag= e
     /rpt_type= OTHER
     /note= "Alu repeat-a (Class J)"
     repeat_unit 1119..1420
    /*tag= f
    /rpt_type= OTHER
/note= "Alu repeat-b (Class Sx)"
FT
    repeat_unit
                  1432..1716
     /*tag= g
     /rpt_type= OTHER
     /note= "Alu repeat c (Class Sb0)"
     repeat_unit
                   1921..2216
     /*tag= h
     /rpt_type= OTHER
     /note= "Alu repeat-d (Class J)"
                    2353..2484
     exon
     /*tage i
     /number= 7
PΨ
     intron
                    2485..3031
    /*tag= j
                    3032..3145
    exon
    /*tag= k
FT
    /number= 8
                    3146...6787
     intron
     /*tag= 1
FT
    repeat unit
                    3973..4268
     /*tag= m
     /rpt_type= OTHER
     /note= "Alu repeat-e (Class Sb0)"
    repeat unit
                  4764..5094
     /*tag= n
     /rpt_type= OTHER
     /note= "Alu repeat-f (Class J)"
     repeat_unit 6072..6362
     /*tag= 0
     /rpt_type= OTHER
     /note= "Alu repeat-g (Class S)"
exon 6788..6934
FT
    /*tag= p
     /number= 9
                    6935..7966
     intron
    /note= "nucleotides 7429-7559 show about 80%
     sequence identity to genomic sequences
     found in 5' regulatory regions, 3'segments,
    or in introns of several genes such as ApoA4,
    Factor VIIIc subunit and G6PD*
    /*tag= q
    repeat unit
                    7164..7427
PΨ
    /*tag= r
   /rpt_type= OTHER
     /note= "Alu repeat-h (Class Sx)"
                    7967..8062
    evon
```

```
/*tag= s
    /number= 10
FT
FΤ
    intron
                   8063...8303
FT
    /*tag= t
                   8304..8342
FΨ
    exon
FT
    /*tag= u
FΤ
    /number= 11
    W09426930-A.
    24-NOV-1994.
    22-APR-1994; U04496
    14-MAY-1993: US-062443.
    (UYJE-) UNIV JEFFERSON THOMAS.
    Canaani E. Croce C:
    WPI: 95-006818/01.
DR
DR
    P-PSDB; R66467
    New acute lymphocytic leukaemia gene prods. - used for the
    diagnosis and treatment of leukaemias, partic. acute
    lymphoblastic or nonlymphoblastic leukaemia
    Example 5; Fig 22; 207pp; English.
    A phage clone, mgll.1, which spans the breakpoint cluster region in
    the ALL-1 gene has been sequenced (075209). Eight Alu repeat
    sequences were identified and classified based on criteria
    published in Milosaylievic et al. (J.Mol.Evol. 32, 105-121, 1991).
    The high concentration of Alu sequences within the area spanned by
    exons 6 and 7 suggested a possible role for Alu in the chromosomal
    translocations involving the ALL-1 gene. Homologous recombination
    is not involved so the Alu repeats may act indirectly by
    destabilising the region.
    Sequence 8342 BP; 2604 A; 1613 C; 1758 G; 2367 T;
                       3.8%; Score 79; DB 13; Length 8342;
 Best Local Similarity 81.1%; Pred. No. 5.73e-35;
 Matches 103; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
   4771 tgcagtggctcacgcctgtaatcccagtactttgggaggctgacgcaggaggaccgcttg 4830
         1590 TGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTTG 1649
    4831 ageteaggagtteaagaceageetgageaceatagtgagaceteatetetaetaaaaaaa 4890
    Dh 4891 aaataaa 4897
         111-111
    1710 AAAAAAA 1716
ID T16333 standard: DNA: 8391 BP.
AC
    T16333:
    29-JUL-1997 (revised)
    06-JUN-1996 (first entry)
    MLL gene 8.3 kb fragment encoding all common translocation breakpoints.
    MLL: myeloid: lymphoid: leukaemia; probe; chromosome; translocation;
    mutation; 11q23; lymphoma; monitoring; ss.
OS
    Homo sapiens.
    US5487970-A.
    30-JAN-1996.
חם
    17-JUN-1992; 900689
    17-JUN-1992; US-900689.
PR
    16-DEC-1992: US-991244.
PR
PR 17-JUN-1993; US-080255.
    (ARCH+) ARCH DEV CORP.
    Diaz MO, Rowley JD;
    WPI: 96-105221/11.
    Detection of 11q23 chromosome translocation(s) - using myeloid/lymphoid
    leukaemia nucleic acid probes, for diagnosis and monitoring of
    leukaemia(s) and lymphoma(s)
    Example 3; Column 49-56; 47pp; English.
    T16333 is an 8.3 kb human genomic DNA BamHI fragment of the human MLL
    (myeloid/lymphoid leukaemia) gene. This sequence contains all of the
CC
CC
    common MLL translocation breakpoints and may be used to map the
    intron-exon boundaries within this region and to identify the
```

Machinerck EST Project
Hathington Macraity School of Medicine
(444 Migraet Marchisty, Box 8501, St. Louis, MO 63108
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(444 Migraet Marchist)
(444 Migraet Marchist)
(444 Migraet Migra 1. .407 /organism="Homo sapiens" /clone="150393" a 104 c 97 g 111 source FEATURES

135 TITITGTATTTTAGTAGAGATGGAGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCC 194 o; Score 87; DB 12; Length 407; Pred. No. 6.15e-107; 0; Mismatches 22; Indels Query Match 4.2%; Best Local Similarity 83.2%; Matches 109; Conservative

5 others

97 g 111 t

90 a

BASE COUNT ORIGIN

Gaps

> c, 셤 Сp 셤

255 ACCGCACCTGG 265

Search completed: Fr1 May 15 18:55:40 1998 Job time : 1929 secs.

1595 ACCGCATGTGG 1585